

SEARCH REQUEST FORM

Requestor's Name: Sally Teng Serial Number: 08/455,683
Date: 7/22/97 Phone: 307-4230 Art Unit: 1812

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

- (1) Please search SER ID NO. 1-4, 11, 12
- (2) Search ligand for opioid receptor
- (3) Search ligand for chimeric opioid recept.

08/292694

05/31/95

OPPIOID RECEPTORS; COMPOSITIONS AND METHODS

BELL, GRAEME I,

STAFF USE ONLY

Date completed: 8-26-97
Searcher: mark
Terminal time: 65
Elapsed time: mp 5
CPU time: _____
Total time: 70
Number of Searches: 1
Number of Databases: 7

Search Site
____ STIC
____ CM-1
____ Pre-S
Type of Search
____ N.A. Sequence
____ A.A. Sequence
____ Structure
____ Bibliographic

Vendors MPSEARCH
____ IG
____ STN
____ Dialog
____ APS
____ Geninfo
____ SDC
____ DARC/Questel
____ Other

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JOURNAL
Biochem. Biophys. Res. Commun. 202 (3), 1431-1437 (1994)
MEDLINE
94338360
REFERENCE
3 (bases 1 to 1154)
AUTHORS
Kieffer, B.
TITLE
Direct Submission
Submitted (18-NOV-1994) Brigitte Kieffer, Ecole Supérieure De
Biotechnologie De Strasbourg, Boulevard Sébastien Brandt, 11kirch
67400, France

FEATURES	Location/Qualifiers
Source	1..1154

CDS

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			Gaps	1
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Qy	340	CTTTGACTTCCGACACACCTTTGAAGGCAAGAGATCATAAATCTGCATCTGGCTGCTGT	399	
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Dp	caactctctcacaactattactctgcatgcctttagcctataccaacagtagctga	976
Qy	caactctctcacaactattactctgcatgcctttagcctataccaacagtagctga	819
Dp	atcccattctctacgccttctttagatgaacactcaagcgtgttcccggaactctct	1036
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Dp	ttccactgaagatgagatgagagcgccaaagcactgacagatccgaataacagttcg	1096
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RESULT	2				
LOCUS	HUMOPRK1B	1604 bp	mRNA	PRI	21-MAR-1995
DEFINITION	Homo sapiens (clone d2-115) kappa opioid receptor (OPRK1) mRNA, complete cds.				

KEYWORDS OPRK1 gene; kappa opioid receptor; opioid receptor.
SOURCE Homo sapiens (clone d2-115) (tissue library: genomic in lambda dash and CDNA in lambda ZAPIT) fetus brain CDNA to mRNA.

Eukaryotae; mitochondrial eukaryotes, Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homiinae; Homo

AUTHORS	TITLE
Zhu, J., Chen, C., Xue, J.-C., Kunapuli, S., Dertel, J.K. and Liu-Chen, L.-Y.	Cloning of a human kappa opiod receptor from the brain

JOURNAL FEATURES	Life Sci. 56, 201-207 (1995)	Location/Qualifiers
		1504

Source

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52

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	Query Match	86.9%	Score 864	DB 82	Length 1604
	Best Local Similarity	98.4%	Pred. No. 0.00e+00		
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QY      220 TTGGGAGATGCTGTGCAAGATAGTAATTTCCATTGATTAACAACATGTCACACAGA 279
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DEFINITION  Human kappa opiod receptor (hKOR) mRNA, complete cds.
ACCESSION   U11053
KEYWORDS    9532059
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

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REFERENCE   1 (bases 1 to 1182)
AUTHORS     Mansson, E., Bare, L.A. and Yang, D.
TITLE       Isolation of a human kappa opiod receptor cDNA from placenta
JOURNAL     Biochem. Biophys. Res. Commun. 202, 1431-1437 (1994)
MEDLINE     9438360
REFERENCE   2 (bases 1 to 1182)
AUTHORS     Mansson, E.
TITLE       Direct Submission
JOURNAL     Submitted (20-JUN-1994) Erik Mansson, Molecular Biology, Ohmeda,
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Best Local Similarity 98.2%; Pred. No. 0.00e+00;
Matches 885; Conservative 0; Mismatches 13; Indels 3; Gaps 1;
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QY      100 GATACCAAGATGAAAGACAGCAACCAATTACATATTAACTGGGCTGGAGAG 159
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RESULT 5
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DEFINITION kappa-opioid receptor [alternatively spliced] [mice, C58/J, R1.1
ACCESSION kappa cells, mRNA Partial, 1288 nt].
S81111
KEYWORDS 91478285
SOURCE Mus sp. C58/J R1.1 thymoma cells.
ORGANISM Mus sp.
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
REFERENCE 1 (bases 1 to 1288)
AUTHORS Belkowski,S.M., Zhu,J., Liu-Chen,L.Y., Eisenstein,T.R., Adler,M.W.
and Rogers,T.J.
TITLE Sequence of kappa-opioid receptor cDNA in the R1.1 thymoma cell
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JOURNAL J. Neuroimmunol. 62 (1), 113-117 (1995)
MEDLINE 96084989
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gidsq 175931] from the original journal article.
This sequence comes from Fig. 3.
COMMENT longer of two transcripts.
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QY 1000 A 1000
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LOCUS MUSKAPOPRE 1410 bp mRNA ROD 13-DEC-1993
DEFINITION Mouse kappa oploid receptor mRNA, complete cds.
ACCESSION U11065
KEYWORDS 9348248
SOURCE kappa oploid receptor.
ORGANISM Mus musculus
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
REFERENCE 1 (bases 1 to 1410)
AUTHORS Yasuda,K., Raynor,K., Kong,H., Breder,C.D., Takeda,J., Reisine,T.
and Bell,G.I.
TITLE Cloning and functional comparison of kappa and delta oploid
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 90, 6736-6740 (1993)
MEDLINE 93342064
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QY	580	ACACCCCTGATGATCTCTGGCTCTCAAGANMGCCGGCTCTTTCGCTCCCGAGACGAAG	639		
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QY	640	ATTNCAACCTCGTGAAGATACACAGATGTGTCGTGGTGGTGGTGGAGCTTTCGTCTCT	699		
Db	927	gttgaaccccatcacactttatctctgtgcgaagctcttaggcagaacctccacagaca	986		
QY	700	GCTGAGATCCCATTCACATATTCATCTCTGGTGGAGGCTCTGGGGAGACATCCACAGCA	759		
Db	987	cagctgtccctcttaagctattactcttcgaatttggcttgggtttatcaccaacagacgttga	1046		
QY	760	CAGCTGCTCTCTCAAGCTATTACTTCTGCACTCGCTTAAGCTATACCAACAGTATGCTTGA	819		
Db	1047	atccctgttctctatgccttcttcttgaataactcaagcgggtgttttaggaactcttgc	1106		
QY	820	ATCCCATCTCTTACGCGCTTCTCTGATGAACACTCAAGCGGTGTTCTCGGGACTCTGCT	879		
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QY	880	TTCACATGAAGATAGNATGGAGGCGNAGAGCACTATACAGAGTCCGAAATACAGTTGAG	939		
Db	1167	atccctgtctcatatgaagatgttgggttggatga--a-taagccagatgtactagttaag	1223		
QY	940	ATCTCGCTTACTCTAGGAGATGATCATGGATGATGATTAACCACTATGACTAGTCTGG	999		
QY	1000	A 1000			

RESULT	9	RATKOR1B	2094 bp	mRNA	ROD	19-NOV-1993
LOCUS		Rattus norvegicus	kappa opioid receptor (KOR-1)	mRNA, complete cds.		
DEFINITION		Rattus norvegicus	kappa opioid receptor (KOR-1)	mRNA, complete cds.		
ACCESSION		L22536				
NID		9425188				
KEYWORDS		G-protein coupled receptor; kappa opioid receptor; transmembrane protein.				
SOURCE		Rattus norvegicus (strain Sprague-Dawley) (library: lambda gt10)				
ORGANISM		Rattus norvegicus				
REFERENCE		1 (bases 1 to 2094)				
AUTHORS		Li, S., Zhu, J., Chen, C., Chen, Y.-W., de Riel, J. K., Ashby, B. and Liu-Chen, L.-X.				
TITLE		Molecular cloning and expression of a rat kappa opioid receptor				
JOURNAL		Biochem. J. 295, 629-633 (1993)				
MEDLINE		94059009				
FEATURES		Location/Qualifiers				
SOURCE		1..2094				
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		/strain="Sprague-Dawley"				
		/dev_stage="adult"				
		/tissue_type="brain (striatum)"				
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		LADLVTTMPGSAVYLMNMPGDIKVIISIDYNMFTSEPTLMSVDRIAY				
		CHPKADLRPRIPKAKINICIMGLASVGS;SAVIGGTGRKVDYEGSLQRPDDE				
		YSMDLPRKICVYFPAFIYPIIIVICTMLIRKSRLLSGSEKRRNIRRTIKYLI				
		LVAVAFTICMTPLHIFLITLVALGDSITSLVLSYFCIALGYNSSLNLYLAFLDL				
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Best Local Similarity	87.1%;	Pred. No. 0.00e+00;				
Matches 785;	Conservative 0;	Mismatches 113;	Indels 3;	Gaps 1;		
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QY	100	gatacacaagaatgaagacagacacacacatttaccattttaaacctggcttggcagatg	159			
Db	539	ctttggttactacacctatgaccttccacagatgctgttactatgaaattcttggcctt	598			
QY	160	ctttgattacctgaacacacagccctttcaagatgacggtctacttgatgaattcttgacctt	219			
Db	599	ttaggagatgttcttgccaagatgtgtcatcttcatttgacactacacacatggtttacacga	658			
QY	220	ttagggagattgctgtgcacagatgatttccatttatttacttgcacacatggtttacacga	279			
Db	659	tattcaccttgaacatgagatgagcttgtagaccgttaccattgcgttgtgccaccctgttgaag	718			
QY	280	tcttacccttggacacatgtagaagcgtgacacgcttaccatttcccggtgtccaccocggtgaag	339			
Db	719	ctttgatttccgaacacctttgaaagaagatcaatcaacatctgcatttggctactg	778			
QY	340	cttttgaccttcgcacaccccttgaagggcaaaagatcatcatatctgcacctggcttcctgt	399			
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QY	400	cgtcatctttagcattcttgcattatgctcttggaaagcaccaaagctcaagggaaggtgtcg	459			
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OY	460	ATGTCATTGAAGTGCCTGCTGTGCACGTATCCCAAGATATATGACTACTCCTGGTGGGAACTCTTCA	519
Db	899	Tgaagatcgtcttcgcttgccttttgctcccttgcttatccctgtcttaatcaatcatgtcgtc	958
OY	520	TGAAGATCGTGCTCTTCATCTTTTGCCTTCGGATGCCCTGTCCCATCATCATGCTGCT	579
Db	959	acaccctatatccttcgctcgcttgaagaagtgcggcgctcctctgggctccagaaagg	1028
OY	560	AACCCGATGATATCCTGGGTCTCAGAANNNGTCGGCTCTTTCTGGCTCCCGAAGAAAG	639
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OY	640	ATTNMAACTCTCGTAGGATCACACAGACGTCGCTGGTGGTGGATGGACGTCTTCGTCGCT	699
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Db	1139	cagctgtccctctcagctattactcttcgatctcgtctgggttatcacacaacagacctga	1198
OY	760	CAGTGCCTCTCTCCAGCATTAATTAATTCGCAATCGGCTTAAGGCTATACCACAAGTAGCTGA	819
Db	1199	atcctgttctctatgacctttcttgatgaaaactccaagcggtgttttagggacttact	1258
OY	820	ATCCCATCTCTATACGCCCTTCTTGATGAAAACCTCAACGCGTGTTCCTGGCACTTCGCT	879
Db	1259	tcccataatgaatcgaaatggagcgccagagacaaaacagattagaacaacagttcagg	1318
OY	880	TTCACCTAATAATAGNAATGGAGCGCANNAGACACTAGCAGAGCTCCGAANATTAAGG	939
Db	1319	atccctgtcttcatagaggatgtgggtggagatga--abaagccagatgtactagtcagg	1375
OY	940	ATCCGCTTACCTTAGGAGATCGATGGAGATGAGAAATAAACCGATATGACTAGTCTGG	999
Db	1376	a 1376	
OY	1000	A 1000	
RESULT	10	RATROR	2481 bp mRNA ROD 02-DEC-1993
LOCUS		Rattus norvegicus	mRNA for kappa opioid receptor, complete cds.
DEFINITION		Accession	D16829
NID		KEYWORDS	kappa opiod receptor.
SOURCE		ORGANISM	Rattus norvegicus
COMMENT			Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Rattus;
REFERENCE			1 (bases 1 to 2481)
AUTHORS			Mihami,M., Toya,T., Katao,Y., Maekawa,K., Nakamura,S., Onogi,T., Kaneko,S. and Satoh,M.
JOURNAL			Cloning and expression of a cDNA for the rat kappa-opioid receptor
MEDLINE			FEMS Letters 329, 291-295 (1993)
COMMENT			Submitted (21-JUL-1993) to DDBJ by: Masabumi Mihami Department of Pharmacology Faculty of Pharmaceutical Sciences Kyoto University Kyoto, Kyoto 606-01 Japan Phone: 075-753-4546 Fax: 075-753-4586
FEATURES			Location/Qualifiers
source			1..2481
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			EDDLPAHISPALPVIITAVIISVFIWVGNSLVNFVIIRTKMTANIKIFNLIA

MEDLINE 95100967
COMMENT Submitted (28-May-1994) to DDBJ by:
Hiroshi Takeshima
Department of Neurochemistry
Tokyo Institute of Psychiatry
2-1-8 Kamikitazawa, Setagaya-ku
Tokyo 156

Japan
Phone: 03-3304-5701 x312
Fax: 03-3329-8035.
Location/Qualifiers
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/clone_id="phage lambda fixit"
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/codon_start=1
/product="kappa-opioid receptor"
/db_xref="pid:g808876"
/translation="MESPLOIFRQDPGPTCSFSAQLPNSSWFPPNAESDSNGVGS
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CHPVKADFERPLAKIINICIMILASVGSIVLGGTKVEDVYIECLQFPDDE
YSWMDLEMKICVVEFAVIVPILITVCTIMIRLKSIVRLSGREKDRMLRTKLV
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28..560
/note="third protein coding sequence (P3)"
/number=3

FEATURES
Source

CDS

exon
/note="third protein coding sequence (P3)"
/number=3

BASE COUNT 141 a 151 g 192 t
ORIGIN Chromosome 1 A2-3.
154 c


Query Match 38.0%; Score 378; DB 89; Length 638;
Best Local Similarity 84.9%; Pred. No. 0.00e+00;
Matches 471; Conservative 0; Mismatches 81; Indels 3; Gaps 2;

Db 20 caggcgaatgtagatgcatgtaatgctgttggaagttctcgtatgataatcctg 79
QY 446 CAGGGAAGGTGCGATGCATGATGAGTGTGCTGCATGCCAGATGATGACTCTCG 505
Db 80 gtggatctctcatgaagatctgtgctgctcttgccttggatccagtcctcat 139
QY 506 GTGGGACCTCTTCATGAGATCTGGCTCTCATCTTGCTTCGATCCGCTCAT 565
Db 140 catcatgtctgtacacacctgatatccgtgacctgaagagtgtccggtcgtctgg 199
QY 566 CATCATGCTGTGCTACACCCGATGATCTGGCTCAAGANMGCCGCTCCTTCTGG 625
Db 200 ctccggagaagaagccgaatctccgcccgaatcccaagctggtgctgtagtagttgc 259
QY 626 CTCCGAGAGAAAGTNNCAACCTGCTAGGATCACAGACTGCTCTGGTGGTGGC 685
Db 260 agtctcatcatctgttgaccocccattcaatcttactcctgtggaagctctggaag 319
QY 686 AGTCTGCTGCTGCTGCTGATCCCATTCACATATTCACTCGGTGAGGCTCTGGGAG 745
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Db 380 caaagagagccctgaatctgttctctatgaccttctgatatgaatccaagcgtgatt 439
QY 806 CAAAGAGAGCCCTGAATCCCATCTCTACGCCCTTCTTGTGTAAGAACTTCAGCGGTGTTT 865
Db 440 tagggactctgtccctattaaatggaatggagccagagcaccaatagagttag 499
QY 866 CCGGACTCTCTCTTCACATGAGATGAGNATGGAGCCGNNAGACACTAGCAGAGTCGG 925
Db 500 aaaaacagttcaagatcctgcttccatgag--agat-gtggagggatgataaagccagt 556
QY 926 AATACAGTTCAAGATCCGCTTACCTGAGGGAGATCATGGGATGATGAATAAACAGT 985
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Search completed: Tue Aug 26 10:55:10 1997
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QY 459 GATGACATGATGATGCTGCTGCTGCAAGTCCAGATGATGACTTACTCTGGTGGAGACCTTTTC 518
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QY 759 ACAGCTGCTCTCTCCAGTATT-ACCTTGTGATGCTGCTTACGCTTACCAAGATGAGCT 817
Db 1237 caaccacagctcttattatgattcttgatgataaacttcaagaatgactcagaagattctg 1296
QY 818 GAATGCCATTCCTGATGAGCTTCTTGTGATGATAAATCTCAAGCGGTCTTCGCGGACTTCTG 877
Db 1297 tatccca 1303
QY 878 CTTTCCA 884

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RESULT 6
ID Q93102 standard; cDNA; 2160 BP.
AC Q93102;
DT 11-DEC-1995 (first entry)
DE Human mu opiate receptor cDNA.
KW Mu opiate receptor; hMOR; opiate agonist; opiate antagonist;
KW drug abuse; analgesic; ds.
OS Homo sapiens.
FH Key
FT CDS Location/Qualifiers
FT CDS 213..1415
FT /tag= a
PN MO9520667-A1.
PD 03-AUG-1995.
PF 30-JAN-1995; U01144.
PR 28-JAN-1994; US-188275.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (USSH) US SEC DEPT HEALTH.
PI Johnson PS, Persico AM, Uhl G, Wang J;
DR WPI: 95-275452/36.
DR P-PSDB; R76780.
PT New DNA encoding human mu opiate receptor - used esp. for screening
PT cpds. for activity as opiate agonists or antagonists
PT Claim 4; Page 24-25; 49pp; English.
CC hMOR cDNA was obt'd. from a human cerebral cortical cDNA library
CC screened with fragments of a rat mu opiate receptor. Cloned hMOR
CC DNA can be used as probes to examine the structure and function of
CC hMOR genes or to screen individuals for susceptibility to drug
CC abuse. Expression in e.g. COS cells allows production of
CC recombinant hMOR1.

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SQ Sequence 2160 BP; 563 A; 566 C; 455 G; 576 T;
Query Match
Best Local Similarity 71.2%; Score 282; DB 15; Length 2160;
Matches 560; Conservative 0; Mismatches 216; Indels 11; Gaps 10;

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Db 501 agatcaccaagatgaaagctgcacacacacatctcatcttcaactcgtctgcgaat 560
QY 99 AGATACACAAAGATGAAAGACACACACACACACATTCATATTTAACTTGGTGGACAGAT 158
Db 561 gccctagccacagatccctgccttccagagtgatgaaattaccatgtaagacagcca 620
QY 159 GCTTAGTACTACAAACATGCGCTTTCAGATTAAGGCTTACTTATGATATCTTGCTT 218
Db 621 ttggaacatcctcttgaagatagtagtctcatagattactaataatggttccacgc 680
QY 219 TTTGGGATGCTGTGCAAGATGATTAATTCATGATTAATTAACATGATTCACAGC 278
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QY 279 ATCTTACCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 338
Db 741 gccctagatttcgcgtactcccccgaatggccaaattatcaatgttctggaactgactc 800
QY 339 GCTTGGACTTCGGCAGACCCCTTGAAGGCAAAAGATCATCAATTCGATCCTGGCTG 398
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QY 399 TCGTATCTGTTGGCACTCTGCAATATCTCTGAGGACCAAAAGTCAGGAGGAGGTGTC 458
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QY 459 GATGCAATGAGTGTGCTGCTTGCAGATTCACAGATGATGATGATGATGATGATGATGATG 518
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QY 519 ATGAAGATCTGCTGCTCATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 578
Db 972 tatgactgatgatcttgagcctcaagaagtgtccgcatgtctctctggtcccaagaag 1031
QY 579 TACACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 638
Db 1032 gacaggaaatcttcgaagagatcacacagagatggtgctgtgtgtgtgtgtgtgtgtc 1091
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QY 699 TCGTGACTGCTCCATTCATATTCATCTGATGAGGCTCTGGGAGACACCTCCACAGC 758
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QY 759 ACAGCTGCTCTCTCCAGTATT-ACCTTGTGATGCTGCTTACGCTTACCAAGATGAGCT 817
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Db 1271 tatccca 1277
QY 878 CTTTCCA 884

RESULT 7
ID Q79199 standard; cDNA; 2070 BP.
AC Q79199;
DT 19-APR-1995 (first entry)
DE Rat mu-subtype opioid receptor cDNA.
KW Mu-subtype opioid receptor; MSOR; drug addiction; ds.
FH Key
FT CDS Location/Qualifiers
FT CDS 83..1154
FT /tag= a

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Db	1027	gacaggaattctgcgcagagatcacccggatgctgctggttgctgctgctgctatattatgc	1086
QY	639	GATNNCAACCTGCGTAGGATCACAGACTGGTCTGGTGGTGGCACTTTCCTCTC	698
Db	1087	tgcctgacccccatcccaatctaaagtatcatcatcaagaagcgtcatcaagattccagaaac	1146
QY	699	TGCTGGAATCCCAATTCAATATTATCTGTTGAGAGCTGTGGGAGCACTCCCAACAGC	758
Db	1147	acatttcgaaccggtttccgcgaactctgcatctgcatctggttggttaagaagaagcgtgcgtg	1206
QY	759	ACAGTGGCTCTCCAGCTATTAATCTTGATGTCATGCTTAGCTTAATCCAAACGTAAGCCTG	818
Db	1207	aatccagttctttaagcgtctccctgagatgaanaattaaagcagatgctctagaagatcttgc	1266
QY	819	AATCCATCTCTCAAGCCTTTCTTGATGAAGAAATTCAACGGTGTCTTCCGGACCTTCGC	878
Db	1267	atccca 1272	
QY	879	TTTCCA 884	

RESULT	5	
ID	Q089223	standard; cDNA; 1618 BP.
AC	Q089223;	
DT	20-OCT-1995	(first entry)
DE	Transcription regulatory protein CDNA.	
KE	Mu opioid receptor; MOR-1; gene therapy; diagnostic;	
KW	transcription regulatory protein; ss.	
OS	Rattus sp.	
EH	Key	Location/Qualifiers
FT	CD5	339..1235
FT	/*tag= a	
PN	W09507983-A.	
PD	23-MAR-1995.	
PF	13-SEP-1994; U10358.	
PF	13-SEP-1993; U5-120601.	
PA	(INDV) UNIV INDIANA FOUND.	
PI	Yu L;	
DR	WPI: 95-131351/17.	
DR	P-PSDB; R71965.	
PT	New nucleic acid encoding new human mu opioid receptor - and	
PT	related vectors, transformed cells, antibodies etc., useful in	
PT	diagnosis, treatment and drug screening.	
CS	disclosure: Page 199-203; 265pp; English.	
CC	A 365 bp fragment of the mouse delta opioid receptor was used to	
CC	screen a rat brain cDNA library under low stringency conditions.	
CC	One positive clone included the sequence given in Q089222, encoding a	
CC	mu opioid receptor, MOR-1 (R71964). Sequence analysis revealed an	
CC	alternating reading frame (Q089223) encoding a zinc	
CC	finger-containing transcription regulatory protein (R71965).	
CC	Sequence 1618 BP; 390 A; 486 C; 370 G; 372 T;	

Query Match	27.9%	Score 277	DB 14	Length 1618
Best Local Similarity	70.2%	Pred. No. 8,096-168		
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				Indels 9
				Gaps 7
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QY	99	AGATACACAAGATGAGACGACGACCAACATTTCATATTTCACCGGCTTGGCGAT	158	
Db	556	gccttagcagacagttacactgccccttcagagtgcacactcgtatgggaatggccc	615	
QY	159	GCTTATTATCTACAAACCATGCCCTTTCAGAGTACGGCTTACTTGATGATTCCTGGCCT	218	
Db	616	tttggacacatcctctcgaagatcgtatctcaataaataactacacaacatgltcacacg	675	
QY	219	TTTGGGATCTGCTGTCACAATATGTAATTCATTATATTCACCAACATGTTCCACAGC	278	

Db	676	atattacacctgtgacacataagaagtggacccgtacatgtgtctgtcgtccaccagaftcaaa	735
QY	279	ATCTTCACCTTATGACCATGATGAGGGTGACCGCTACATTCACCTCCGGTGTGCCACCCCGTGAAG	338
Db	736	gccctggattccgtgaacccccgaatgpccaaatgtgaactgtcgaactgtgaccc	795
QY	339	GGTTTGGACTTCGGACACCTTTGAGGCAAAATCATATCTGCAATCTGACCTG	398
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QY	399	TGCTATCTGTTGGCATCTCTGCAATATGCTTTGGAGGCAOAAAGTCAAGAGAGGTG	458
Db	855	catag-attgcaacct-cagttct-cccaccacaac--ctgtactgtggagaaacctgtc	909
QY	459	GATTCATCTTGAAGTGCTGCTTGCAGTCCCAATGATGATCACTACCTGCTGGACCTTTC	518
Db	910	a--aa-alcctgtcttatcttctgcttctcatctgacgtacccatccatcaatctgtgt	966
QY	519	ATGAGAGATGTGGGTATTATGTTTGCTTGTAATCCCTCTCTCATCATATCGCTG	578
Db	967	tctggcctcgtatgattcttagcagctcaagaagcgttgcacgtcatcgtggtccacaagaag	1021
QY	579	TACACCCGTGAATGACCTGCGCTCCAAANNATCCGGCTCTCTCTGCTGCCGCCAGAGAA	638
Db	1027	gacagaatctgcgcagagatcacaccggaatgtgtgtgtgtgtgtgtatctatctgc	1081
QY	639	GATNNCACCTGCGCTAGGATACACAGACTGCTGTGTGTGTGGCAATCTTCGTCGTC	698
Db	1087	tgtctgacccccatccacatctactgtatcatcatcaagaagctgtgtaacagattccagaac	1147
QY	699	TGCTGAGCTCCCATTCACATATTATCTGTTGAGAGCTTGGGAGCAACCTCCACAC	758
Db	1147	aaatttcagaccgtttctctgtgcaactctgtcatgtgtgtgtgtgtaacgaacagctgtc	1207
QY	759	ACAAGTCTCTTCCAACTATTAATCTTGATGGCTTGGGCTAATACCAACAGTAGCGTG	818
Db	1207	aatcagttctttagcgtcttccttgatgaagaacttaacagatgtcttgagaagtcttc	1267
QY	819	AATCCCATCTGCTACGGCTTCTTTGATGAGAAATTCATCAAGCGGTGTTCCGGAATCTTCTG	878
Db	1267	atccga 1272	
QY	879	TTTCCA 884	

RESULT	10	
ID	Q56700	standard; cDNA; 1821 BP.
AC	Q56700;	
DT	15-SEP-1994	(first entry)
DE	Sequence of murine delta opioid receptor in the DOR-1 cDNA clone.	
KW	Opioid receptor; morphine; opiate; ss.	
OS	Mus musculus.	
EH	Key	Location/Qualifiers
FT	CDS	29..1139
FT	/*tag= a	
PN	W09404552-A.	
PD	03-MAR-1994.	
PF	13-AUG-1993; U07665.	
PR	13-AUG-1992; U5-929200.	
PA	(RECC) UNIV CALIFORNIA.	
PI	Edwards RH, Evans CT, Kaufman D, Keith DE;	
DR	WPI; 94-083099/10.	
DR	P-PSDB; R48629.	
PT	DNA encoding opioid receptors and antibodies against this	
PT	receptor - used to express and locate these receptors, and	
PT	cpgs. for opioid (ant)agonist activity	
PS	claim 1: fig 5, 7app. English.	
CC	A cDNA library was constructed using mRNA isolated from the NG109-15	
CC	cell line. A single clone, named the DOR-1 clone was isolated.	
CC	Comparisons with known sequences in GenBank showed highest homology	
CC	between DOR-1 and the G-protein-coupled somatostatin receptor. Other	
CC	features of the DOR-1 clone RA sequence deduced from the cDNA	
CC	sequence include 3 consensus glycosylation sites at residues 18 and	

CC 33 (predicted to be in the extracellular N-terminal domain), and at
 CC residue 310 (close to the C-terminus and predicted to be
 CC intracellular). Phosphokinase C consensus sites are present within
 CC predicted intracellular domains, at residues 242,255, 344 & 352.
 CC Seven putative membrane-spanning regions were identified. The DOR-1
 CC clone produces a delta receptor with a predicted mol. wt. of 40,558
 CC kDaltons prior to post-translational modifications.
 SQ Sequence 1821 BP; 339 A; 559 C; 541 G; 382 T;

Query Match 26.7%; Score 265; DB 10; Length 1821;
 Best Local Similarity 70.6%; Pred. No. 1,816-159;
 Matches 550; Conservative 0; Mismatches 217; Indels 12; Gaps 10;

Db 257 tacacccaattgaagaccgcccacacacatactacatcttaactctgtgcttgcgtatgcg 316
 |||||
 QY 102 TACACAAGATGAGAGACAGCAACCAACATTTACATTTAACTGGCTTTGGCAGATGCT 161
 |||||
 Db 317 ctggccacacagacgctcccttccagagcgccaaagtactgtatggaagcgtggccgttt 376
 |||||
 QY 162 TTAGTTACTACAAACCATCCCTTTGAGAGTACGGTCTACTGTGATGATTAATTCCTGGCTTTT 221
 |||||
 Db 377 ggcgagcgtcgtgcaagcgtcgtctcccaattgactactacaatgttcaatgacatc 436
 |||||
 QY 222 GGGGATGTCGCTGCAATAGTAATTTCCATTTGATTTACATGATGTCACGACATC 281
 |||||
 Db 437 ttacacctacacatgatagagcgtggaacgtacattgctgtctgccatcctgtcaaacgc 496
 |||||
 QY 282 TTACCTTGACCATGATGATGAGCGTGGACCGCTACATTTGCCGTGGTGGACCCCTGGAAGGCT 341
 |||||
 Db 497 ctggacttccggaacccacgaagcgaagcgtatcaatataatgatactgtgcttgcgt 556
 |||||
 QY 342 TTGGACTTCCGACACCCCTTGAAAGCAAGATCAATCAATCTGATCTGGCTGCTGTG 401
 |||||
 Db 557 tcaagttgcgggtcccccacatggtlcatgagcagtgaccaccccgagatgctgacgtg 616
 |||||
 QY 402 TCATCTGTTGGGATCTCTGCCATAGTCCCTGAGAGGACCAAGTCAAGGAAAGTGTGCAT 461
 |||||
 Db 617 gt-atgca-tgct-c--cagttcccc-a-g-tcccaagctgtactggaacactgtgacc 667
 |||||
 QY 462 GTCATTTGATGATGCTGCTGTGATGCCAGATGATGATGATCTGCTGGTGGGACCTCTTCATG 521
 |||||
 Db 668 aagatctggtgttctccttctgtccttgcgtgtggtgcgcgatctcatatccacgtgtgcgat 727
 |||||
 QY 522 AAGATCTGGGTTTATCTTTGCTTCGTCGATGCCCTGCTCATATCAATGCTTCTGCTAC 581
 |||||
 Db 728 ggcctcatgctactgagcgtcgcagcgtgctctgctgtccggttccagaggaaagagac 787
 |||||
 QY 582 ACCCTGATATCTCTGGCTCAAGANNGCCGGCTCTTTCGGCTCCGAGAGAAAGAT 641
 |||||
 Db 788 cgcagcctgcggagcatcaagcgcgatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgc 847
 |||||
 QY 642 NNCAACCTGCTAGAGATACCAAGACAGTGGTCTGGTGGTGGTGGTGGTGGTGGTGGTGG 701
 |||||
 Db 848 tggggggcccatcacactctgtctcatcgtctgtgagcgtgtgagacatcaatcgcgagac 907
 |||||
 QY 702 TGGACTCCCATTTACATTTATTCATCTGCTGGAGGCTCTGGGAGACCTCCACACAC-AC 760
 |||||
 Db 908 caactgtgtgtgcgcgcacatgacactgtgcatgctgtggtgacgacacagcagcagcctc 967
 |||||
 QY 761 AG-CTGCTCTCCACAGTMT-ACCTCTGATGCTTGGCTTATGACATACAGTACCTG 818
 |||||
 Db 968 aacccggtctctacgcttccctgtgagcaggaacttaagcgcgtctcgcgcagcgtctg 1026
 |||||
 QY 819 AATCCATTTCTACGCCCTTTCTTGTGATAAACTTCAAGCGGTGTTCGGGGACTTCTG 877
 |||||

RESULT 11
 ID 056705 standard; cDNA; 1981 BP.
 AC 056705;
 DT 15-SEP-1994 (first entry)
 DE Partial sequence of the murine mu-receptor clone DOR-2
 DE (MOR-1, MOR-1alpha)
 KW Opioid receptor; morphine; opiate; ss.

OS Mus musculus.
 PN W09404552-A.
 PD 03-MAR-1994.
 PF 13-AUG-1993; 007665.
 PR 13-AUG-1992; US-929200.
 PA (REGC) UNIV CALIFORNIA.
 PI Edwards RH, Evans CJ, Kaufman D, Keith DE;
 DR WPI; 94-083099/10.
 PT DNA encoding opioid receptors and antipodles against this
 PT receptor - used to express and locate these receptors, and screen
 PT cpls. for opiod (ant)agonist activity
 PS Example; Fig 9; 74pp; English.
 CC A cDNA library prep. from mouse brain was probed using DOR-1 (see
 CC 056704) as a probe. One clone was recovered and sequenced. This
 CC clone, designated DOR-2, represented a new gene. DOR-2 hybridised
 CC to a different pattern of neurons than did DOR-1 and showed greater
 CC labeling of the striatum. The identity of DOR-2 (mOR-1) as that of
 CC a mu receptor was confirmed.
 SQ Sequence 1981 BP; 499 A; 549 C; 436 G; 496 T;

Query Match 26.7%; Score 265; DB 10; Length 1981;
 Best Local Similarity 69.5%; Pred. No. 1,816-159;
 Matches 546; Conservative 0; Mismatches 231; Indels 9; Gaps 7;

Db 538 agatataccaanaatgaagactgcccacacacatctacatcttcaacttgcctgtgcagat 597
 |||||
 QY 99 AGATACACAAAGATGAGAGACAGCAACCAATTTACATATTTAACTGGCTTTGGCAGAT 158
 |||||
 Db 598 ggcctgagcactagacgctgccccttccagatgttgaactacactgtatggaagcgtggccc 657
 |||||
 QY 159 GCTTTAGTTACTACAAACCATGCCCCCTTCCAGATGAGTACGGTCTACTGTGATGATTAATTCCTGGCCT 218
 |||||
 Db 658 ttggaacaatcctctcgaagatcgtatctcaatagactactacaatctgttccagct 717
 |||||
 QY 219 TTTGGGATGTTGCTGTGAAAGATAGTAATTTCCATTTGATTTACTACAAATGTTCCACGC 278
 |||||
 Db 718 attctacacctctgacacatgagtgtagacgctacatgcccgtctgcacccggttcaag 777
 |||||
 QY 219 ATCTTACCTTGACCATGATGAGCGCTGAGACCGCTTCAATTTGCCGTGTGGACCCCGTGAAG 338
 |||||
 Db 778 gccctggaattccgtaaccccccgaatgccaatgttcaatgctgtgaactgtgactc 837
 |||||
 QY 339 GCTTTGGAATTCGACACACCCCTTGAAGGCAAGATCAATATGCAATCTGCGTGGCTG 398
 |||||
 Db 838 tctctgcacatggtgctgcgcgttaattgtcaatgagcacaacaaataaagagag-gtc 896
 |||||
 QY 399 TCGTATCTGTGGCATCTCTGCAATAGTCTTGAAGGCAACCAAGTCAAGGAAAGTGTG 458
 |||||
 Db 897 catag-attgacacct-ca-c-gttctctcatccacatgatactgtagagacgtgtc 951
 |||||
 QY 458 GATGTCATTTGATGCTGCTGTGCAAGTTCACAGATGATGATGATGATGATGATGATGATGATG 518
 |||||
 Db 952 a--aa-atcgtgtcttcaatcttcgacctcatcatcagcgggacctcaatcaatgtgtgt 1008
 |||||
 QY 519 ATGAAGATCTGGCTGCTTCACTTTGCTTCGTGATGCCCTGCTCTCATATCAATGCTCTG 578
 |||||
 Db 1009 tatgagctatgatatcttaagcttaagagtggtccgcatgctgttcgggtcccaaaaag 1068
 |||||
 QY 579 TACACCTGATATCTCTGCTGCTCAAGANNGCCGGCTCTTTCGGCTCCGAGAGAAA 638
 |||||
 Db 1069 gaaggaacctgcgagagatcaaccggatggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1128
 |||||
 QY 639 GATNNAACTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 698
 |||||
 Db 1129 tcttgagcccccacatcacatctatgtcatcatcaaaagcaactgtatcaagatccagaac 1188
 |||||
 QY 699 TGGTGGACTCCCATTCATCATATTCATCTGAGAGGCTCTGGGGAGCACTCCCAACAC 758
 |||||
 Db 1189 actttccagactgttccgtgacactctgcatgactgtgtgtgtgtgtgtgtgtgtgtgtgt 1248
 |||||
 QY 759 ACAGCTGCTCTCTCCAGCATTTATCTTCTGTGATGCTTGAAGCTTATACCAACATAGCTG 818
 |||||
 Db 1249 aaccagttcttatgtgttccctgtgataaacttcaacagatgttttagagagttctgc 1308
 |||||

Matches 549; Conservative 0; Mismatches 215; Indels 15; Gaps 12;

Db 287 taaccaaatgtgaagccgcaccacaacatctacatctcaatctgtgctgtgtgtg 346
 |||||
 QY 102 TACACAAAGATGAGACAGACAGAACCAATTTATTAATTAAGTGGATTGGACATGCT 161
 |||||
 Db 347 ctgcaacacagcagcgtccctccagagcgccagtaactgtatgtgaacgtgtgcgttt 406
 |||||
 QY 162 TTAGTACTACATCAACCAAGCCCTTTCAGAGTACGGTCTACTGTATGAAATTCCTGCGCTTTT 221
 |||||
 Db 407 gggagctgtgtgtgaaggtgtgtgtctccatctgactactacaactgttctactagc 466
 |||||
 QY 222 GGGAGTGTGCTGGACAGATAGTAAATTCATTGATTACTACAACTGTTCCACCAAGATC 281
 |||||
 Db 467 ttaccctcacatgatgatgagcgtggaaccgttaattgtctgtccatccctgtcaaac 526
 |||||
 QY 282 TTACACCTTGACATGATGAGACGCTGAGACCGCTACATTCGCTGTGCGCACCCCGTGAAGCT 341
 |||||
 Db 527 ctggaactccggaacacacgaagggccagcgtatcaatataatgtatcgtgtgtgt 586
 |||||
 QY 342 TTGGACTTCCGACACCCCTTGAAGGCAAAAGATCATATATCTGCATCTGCGCTGTG 401
 |||||
 Db 587 tcagggt 645
 |||||
 QY 402 TCAATCTTGGACATCTTGCATATAGTCTTGGAGGACCAAGTCAAGGGAAGTGTGAT 461
 |||||
 Db 646 gt-atgca-tgct-c---cagttcccaagtcacg-ctgtgtactgtgac--ac-tgtg-acc 694
 |||||
 QY 462 GTCACTTGAAGTGTGCTTGCAGATTCCAGATGATGACTACTCTGTGTGGACCTCTCATG 521
 |||||
 Db 695 aagatctgt 754
 |||||
 QY 522 TAAATCTGCGCTGTGATCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT 581
 |||||
 Db 755 gggctcgt 814
 |||||
 QY 582 ACCCTGATGATCTGCTGTCTCAAGANNCTCGGCTCTCTTGTGCTTCCGAGAAAGAT 641
 |||||
 Db 815 cgcagcgtcgc 874
 |||||
 QY 642 NMCAACCTGCGTGAAGATCACACAGACTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 701
 |||||
 Db 875 tggagc 934
 |||||
 QY 702 TGGACTCCCATTCACATATTCATCTGTGTGAGGCTCTGGGAGACCTCCACAGC-AC 760
 |||||
 Db 935 ccaattgt 994
 |||||
 QY 761 AG-CTGCTCTCTCCAGCTATT-ACCTTGTGATCGCCTTAGGCTATACCAAGATAGCTG 818
 |||||
 Db 995 aaccggttctctacgc 1053
 |||||
 QY 819 AATCCATCTCTACGCGCTTCTCTGTATGAAAACTCAAGCGGTGTTCCGGACTTCTG 877
 |||||

RESULT 14
 ID Q56703 standard; DNA; 829 BP.
 AC Q56703;
 DT 15-SEP-1994 (first entry)
 DE Partial sequence of the human mu oploid receptor
 DE genomic clone H20 (MORF).
 KW Opioid receptor; morphine; opiate; ss.
 OS Homo sapiens.
 PN W0940452-A.
 PD 03-MAR-1994.
 PR 13-AUG-1993; U07665
 PR 13-AUG-1992; US-929200.
 PA (RBCG) UNIV CALIFORNIA.
 PI Edwards RH, Evans CJ, Kaufman D, Keith DE;
 DR WPI; 34-083099/10.
 PT DNA encoding opioid receptors and antibodies against this
 PT receptor - used to express and locate these receptors, and screen
 PT cpts. for opioid (ant)agonist activity

PS Example: Fig 8c; 74bp; English.
 CC To isolate opiate receptor genomic clones, 300,000 human genomic
 CC clones and a similar number of mouse genomic clones were probed
 CC with the 1.1 kb mouse delta oploid receptor clone DOR-1 pSV/XbaI
 CC fragment. One mouse clone and three human genomic clones were
 CC isolated. The 3 human clones had very different EcoRI patterns
 CC which indicated that three different genes were represented by the
 CC human genomic clones which were designated H3, H14 and H20. H20 maps
 CC to chromosome 6. It encodes the human mu receptor. In addition, H20
 CC appears to contain a CACACA marker (Q56704) which provides a means
 CC to track the inheritance of this gene.
 SQ Sequence 829 BP; 182 A; 205 C; 134 G; 214 T;

Query Match 24.6%; Score 245; DB 10; Length 829;
 Best Local Similarity 63.3%; Pred. No. 1,40e-145;
 Matches 504; Conservative 0; Mismatches 279; Indels 13; Gaps 12;

Db 6 ttatctcctagatcacccaagatgaagactgcccacacacatcttcaacctgtct 65
 |||||
 QY 90 TTTCTTTTATGATACCAAAAGATGAAGACGACACCACTTATCATATTTAAGTGGCT 149
 |||||
 Db 66 ctg-cagatgccttagacacacagataccctgtccctccagaggtgtaattacctatgga 124
 |||||
 QY 150 TTGGAGATGCTTTAGTTACTTACCAACCATGCCCCCTTCAGAGTACGGTCTGATGAAT 209
 |||||
 Db 125 acatgtgcattgtggaacctcccttgcaagatagtgtctccatagattactatacatg 184
 |||||
 QY 210 TCGTGCGCTTTGGGGATGCTGTGACAGATGATATTTCCATGTATTTCTACACATG 269
 |||||
 Db 185 ttaccagcatattcacccctcgcacatagtggtgtatcgatacatgtgagtcgtcac 244
 |||||
 QY 270 TTACACGACGATCTTACCTTGACCATGATGAGCGTGACCGCTACATTCGCGTGTGCAC 329
 |||||
 Db 245 octgtcaagccttagatcttcgctacccnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 304
 |||||
 QY 330 CCGGTGAAGCGCTTGGGCTTCCGACACCCCTGAAGGCAAAAGATCATCAATATCTGCATC 389
 |||||
 Db 305 nnn 364
 |||||
 QY 390 TGGCTGCTGTGCTGATCTGTGGCATCTTGCAATAGTCTTGGAGGACCAAGTCAAG 449
 |||||
 Db 365 nnnngt-tccatag-atgt--taca-ctaaac-ttctctcaaccaactgttactgtg-ga 417
 |||||
 QY 450 GAAAGTGTGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 509
 |||||
 Db 418 aaac-ctgc-tgaagatctgtgtttcatcttgccttcaatataagccaagtgctcatat 475
 |||||
 QY 510 GACCTCTTCATGAAGATCTGCTCTTCATCTTTCCTTCGATCCCTGCTCATATC 569
 |||||
 Db 476 accgtgtgtatgtgacgtatcttgcgcctcaagagtgcgcgcatgtctctcgtgtcc 535
 |||||
 QY 570 ATGCTGTGCTACACCTGATATCTGCTGTCAAGANNNGCGGCTCTTCTGCGCTCC 629
 |||||
 Db 536 aaagaaagagcaggaactctcgaaggatcacacagatgtgtgtgtgtgtgtgtgtgt 595
 |||||
 QY 630 CGAGGAAGAAAGATNNCAACCTGCTAGATCACAGACTGCTGTGTGTGTGTGTGTGTGT 689
 |||||
 Db 596 ttcaatgtctgt 655
 |||||
 QY 690 TTGCTGTCTCTGTGACCTCCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 749
 |||||
 Db 656 ccagaaactac-gttccagagctgttctgtgcaactctgcatgtgtgtgtgtgtgtgtgt 714
 |||||
 QY 750 TCCACACACACAGCTGCTCTCTCCAGCTATT-ACCTTGTGATCGCCTTAGGCTATACCA 808
 |||||
 Db 715 cagctgcctcaaccagctcttlatgcatlcttgatgataaactcca-cgatgctttag 773
 |||||
 QY 809 CAGTAGCTGATGATCCATTCCTACGCTTCTTGTATGAAAACTCAAGCGGTGTTCCG 868
 |||||
 Db 774 agagttcgtatcca 789
 |||||
 QY 869 GGAATCTGCTTCCA 884
 |||||

RESULT 15
 ID Q56702 standard; DNA; 2447 BP.
 AC Q56702;
 DI 15-SEP-1994 (first entry)
 DE Partial sequence of the human kappa opioid receptor
 DE genomic clone H14 (KORa).
 KW Opioid receptor; morphine; opiate; ss.
 OS Homo sapiens.
 PN W09404552-A.
 PD 03-MAR-1994.
 PF 13-AUG-1993;
 PR 13-AUG-1992; U5-929200.
 PA (R58C) UNIV CALIFORNIA.
 PI Edwards RH, Evans CJ, Kaufman D, Keith DE;
 DR WPI: 94-083099/10.
 PT DNA encoding opioid receptors and antibodies against this
 PT receptor - used to express and locate these receptors, and screen
 PT cpos. for opioid (antagonist activity
 PS Example; Fig 8b; 74bp; English.
 CC To isolate opiate receptor genomic clones, 300,000 human genomic
 CC clones and a similar number of mouse genomic clones were probed
 CC with the 1.1 kb mouse delta opioid receptor clone DOR-1 Pst/XbaI
 CC fragment. One mouse clone and three human genomic clones were
 CC isolated. The 3 human clones had very different EcoRI patterns
 CC which indicated that three different genes were represented by the
 CC human genomic clones which were designated H3, H14 and H20. H14 maps
 CC to chromosome 8. It encodes the human kappa opioid receptor.
 Sequence 2447 BP; 683 A; 512 C; 498 G; 747 T;

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Db 147 flltmsvdyiaavchpkaaldftplkaklincivlsssvgisaiivgtkvtredvd 206
| | | | |
QY 61 flltmsvdyriaavchpkaaldftplkaklincivlsssvgisaiivgtkvtredvd 120
| | | | |
Db 207 vlcslgfpdddygswdlfmkicvfaivpvlilivcytlmlrlksvrlisgsrekd 266
| | | | |
QY 121 vlcclqfpdddygswdlfmkicvfaivpvlilivcytlmlrlksvrlisgsrekd 180
| | | | |
Db 267 nlrtrrlvlyvavfvcwtpihifilvealgstshstaalsyyfciatlgynssln 326
| | | | |
QY 181 xnlrtrrlvlyvavfvcwtpihifilvealgstshstaalsyyfciatlgynssln 240
| | | | |
Db 327 pilyafidenfkrcfdcfipkmergstrvntvqdaylridgm-nkpv 380
| | | | |
QY 241 pilyafidenfkrcfdcfipkmergstrvntvqdaylridgm-nkpv 295
| | | | |

RESULT 2
ENTRY 157005 #type complete
TITLE kappa opiod receptor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
07-Jul-1996

ACCESSIONS 157005
REFERENCE 157005
#authors Zhu, J.; Chen, C.; Xue, J.
#journal Life Sci. (1995) 56:201-207
#title Cloning of a human kappa opiod receptor from the brain.
#accession 157005
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-380 #label RRS
#cross-references GB:137362; NID:9722617; CDS_PTD:9722618

GENETICS
#note gene name OPRK1
SUMMARY #length 380 #molecular_weight 42645 #checksum 8302

Query Match 98.3%; Score 2192; DB 13; Length 380;
Best Local Similarity 97.6%; Pred. No. 0.00e+00;
Matches 288; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

Db 87 ytkmktatniyifnlaladavltttmpfgstvyjmswvpgdvclkiyisidymnftsi 146
| | | | |
QY 1 ytkmktatniyifnlaladavltttmpfgstvyjmswvpgdvclkiyisidymnftsi 60
| | | | |

Db 147 flltmsvdyriaavchpkaaldftplkaklincivlsssvgisaiivgtkvtredvd 206
| | | | |
QY 61 flltmsvdyriaavchpkaaldftplkaklincivlsssvgisaiivgtkvtredvd 120
| | | | |

Db 207 vlcslgfpdddygswdlfmkicvfaivpvlilivcytlmlrlksvrlisgsrekd 266
| | | | |
QY 121 vlcclqfpdddygswdlfmkicvfaivpvlilivcytlmlrlksvrlisgsrekd 180
| | | | |

Db 267 nlrtrrlvlyvavfvcwtpihifilvealgstshstaalsyyfciatlgynssln 326
| | | | |
QY 181 xnlrtrrlvlyvavfvcwtpihifilvealgstshstaalsyyfciatlgynssln 240
| | | | |

Db 327 pilyafidenfkrcfdcfipkmergstrvntvqdaylridgm-nkpv 380
| | | | |
QY 241 pilyafidenfkrcfdcfipkmergstrvntvqdaylridgm-nkpv 295
| | | | |

RESULT 3
ENTRY A55259 #type complete
TITLE kappa opiod receptor - guinea pig
ALTERNATE_NAMES dynorphin receptor
ORGANISM #formal_name Capra porcellus #common_name guinea pig
DATE 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change
06-Feb-1995

ACCESSIONS A55259
REFERENCE A55259
#authors Xie, G.; Meng, F.; Mansour, A.; Thompson, R.C.; Hoversten,

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#journal M.T.; Goldstein, A.; Watson, S.J.; Akil, H.
#title Proc. Natl. Acad. Sci. U.S.A. (1994) 91:3779-3783
#accession Primary structure and functional expression of a guinea pig
A55259 kappa opiod (dynorphin) receptor.
#status preliminary
#molecule_type mRNA
#residues 1-380 #label XIE
#cross-references GB:U04092
KEYWORDS transmembrane protein
SUMMARY #length 380 #molecular_weight 42736 #checksum 7081

Query Match 96.8%; Score 2157; DB 14; Length 380;
Best Local Similarity 94.6%; Pred. No. 0.00e+00;
Matches 279; Conservative 10; Mismatches 5; Indels 1; Gaps 1;

Db 87 ytkmktatniyifnlaladavltttmpfgstvyjmswvpgdvclkiyisidymnftsi 146
| | | | |
QY 1 ytkmktatniyifnlaladavltttmpfgstvyjmswvpgdvclkiyisidymnftsi 60
| | | | |

Db 147 flltmsvdyriaavchpkaaldftplkaklincivlsssvgisaiivgtkvtredvd 206
| | | | |
QY 61 flltmsvdyriaavchpkaaldftplkaklincivlsssvgisaiivgtkvtredvd 120
| | | | |

Db 207 vlcslgfpdddygswdlfmkicvfaivpvlilivcytlmlrlksvrlisgsrekd 266
| | | | |
QY 121 vlcclqfpdddygswdlfmkicvfaivpvlilivcytlmlrlksvrlisgsrekd 180
| | | | |

Db 267 nlrtrrlvlyvavfvcwtpihifilvealgstshstaalsyyfciatlgynssln 326
| | | | |
QY 181 xnlrtrrlvlyvavfvcwtpihifilvealgstshstaalsyyfciatlgynssln 240
| | | | |

Db 327 pilyafidenfkrcfdcfipkmergstrvntvqdaylridgm-nkpv 380
| | | | |
QY 241 pilyafidenfkrcfdcfipkmergstrvntvqdaylridgm-nkpv 295
| | | | |

RESULT 4
ENTRY A48227 #type complete
TITLE kappa opiod receptor 1 - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 26-May-1994 #sequence_revision 26-May-1994 #text_change
27-Oct-1995

ACCESSIONS A48227
REFERENCE A48227
#authors Yasuda, K.; Raynor, K.; Kong, H.; Breder, C.D.; Takeda, J.;
Reisine, T.; Bell, G.I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1993) 90:6736-6740
#title Cloning and functional comparison of kappa and delta opiod
receptors from mouse brain.
#accession A48227
#status preliminary
#molecule_type mRNA
#residues 1-380 #label YAS
#cross-references GB:U11065
REFERENCE J04138
#authors Liu, H.C.; Lu, S.; Augustin, L.B.; Felsheim, R.F.; Chen,
H.C.; Loh, H.H.; Wei, D.N.
#journal Biochem. Biophys. Res. Commun. (1995) 209:639-647
#title Cloning and promoter mapping of mouse kappa opiod receptor
gene.
#accession J04138
#molecule_type mRNA
#residues 1-380 #label LIU
#note The authors translated the codon CAG for residue 365 as
Glu

COMMENT This receptor exists in different areas of the central and
peripheral nervous systems, and mediates many physiological and
pharmacological effects of opiates and opiod compounds.

GENETICS
#gene kor
#keywords brain; G protein-coupled receptor; glycoprotein; opiod
peptide; phosphoprotein; transmembrane protein

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SUMMARY #length 380 #molecular-weight 42652 #checksum 9937

Query Match 95.8%; Score 2136; DB 14; Length 380;
 Best Local Similarity 92.9%; Pred. No. 0.00e+00;
 Matches 274; Conservative 13; Mismatches 7; Indels 1; Gaps 1;

Db 87 ytkmktatniyifnlaladalavttttmpfgsavylnmswpgfvtckivtsidymmtsi 146
 QY 1 YTKMKTATNIYIFNLADALAVTTTTFPGSTVYLNMSWPGVLCIKIVISIDYNNMTSI 60
 Db 147 ftltmsvdyriavchpykaidfrtprlkakiniiciwilaasvgsaisaivlgtkvredvd 206
 QY 61 FTLTMSVDRIYAVCHPYKALDFRTPRLKAKIINICIMWLLSSVGSISAIYVGGTKVREDVD 120
 Db 207 vlcslqfddeswvdlfmkicvtfafvpylilivcytlmllrlksvrlssgredk 266
 QY 121 VIECLQFPDDDYSWVDLFMKICVFIFAFVLPVLIIVCYTLMILRLKXVRLSSGREKD 180
 Db 267 nrlrttklrvlvaavfllcwtpihlflvealgstshstaissyficalgytnssln 326
 QY 181 NXLRRITRLVLYVAVFWCWPPIHIFLVEALGSTSHSTAALSSYFICIALGYTNSSLN 240
 Db 327 pvlvafidenkrcfridcfipkmergstrvrvntvqdpasmdygm-nkpy 380
 QY 241 PVLVAFIDENKRCFRIDCFIPKMERGSTSRVNVQDPAYVREIDGMANKPY 295

RESULT 5 #type complete
 ENTRY S36143
 TITLE kappa opioid receptor - rat
 ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
 DATE 10-Dec-1993 #sequence_revision 19-Oct-1995 #text_change 05-Sep-1996

ACCESSIONS S36143; S38825; S36102; S39015; A48789
 S36143
 #authors Nishi, M.; Takeshima, H.; Fukuda, K.; Kato, S.; Mori, K.
 #journal FEBS Lett. (1993) 330:77-80
 #title cDNA cloning and pharmacological characterization of an
 opioid receptor with high affinities for
 kappa-subtype-selective ligands.
 #accession S36143
 #status Preliminary
 #molecule_type mRNA
 #residues 1-380 #label NIS

REFERENCE S38825
 #authors Chen, Y.; Westek, A.; Liu, J.; Yu, L.
 #journal Biochem. J. (1993) 295:625-628
 #title Molecular cloning of a rat kappa opioid receptor reveals
 sequence similarities to the mu and delta opioid receptors.
 #accession S38825
 #status Preliminary
 #molecule_type mRNA
 #residues 1-380 #label CHE

REFERENCE S36102
 #authors Minami, M.; Toya, T.; Katao, Y.; Maekawa, K.; Nakamura, S.;
 Onogi, T.; Kaneko, S.; Satoh, M.
 #journal FEBS Lett. (1993) 329:291-295
 #title Cloning and expression of a cDNA for the rat kappa-opioid
 receptor.
 #accession S36102
 #molecule_type mRNA
 #residues 1-41, 1-43-380 #label MIN

REFERENCE S39015
 #authors Li, S.; Zhu, J.; Chen, C.; Chen, Y.W.; Deriel, J.K.; Ashby,
 B.; Liu-Chen, L.Y.
 #journal Biochem. J. (1993) 295:629-633
 #title Molecular cloning and expression of a rat kappa opioid
 receptor.
 #accession S39015
 #molecule_type mRNA
 #residues 1-344, 1-346-380 #label LIS

REFERENCE A48789

#authors Meng, F.; Xie, G.
 #journal Proc. Natl. Acad. Sci. U.S.A. (1993) 90:9954-9958
 #title Cloning and pharmacological characterization of a rat kappa
 opioid receptor.
 #cross-references M01D:94052210
 #accession A48789
 #status Preliminary; translated from GB/EMBL/DBJ
 #molecule_type mRNA
 #residues 1-380 #label RES

SUMMARY #length 380 #molecular-weight 42688 #checksum 9972

Query Match 95.6%; Score 2132; DB 14; Length 380;
 Best Local Similarity 92.5%; Pred. No. 0.00e+00;
 Matches 273; Conservative 13; Mismatches 8; Indels 1; Gaps 1;

Db 87 ytkmktatniyifnlaladalavttttmpfgsavylnmswpgfvtckivtsidymmtsi 146
 QY 1 YTKMKTATNIYIFNLADALAVTTTTFPGSTVYLNMSWPGVLCIKIVISIDYNNMTSI 60
 Db 147 ftltmsvdyriavchpykaidfrtprlkakiniiciwilaasvgsaisaivlgtkvredvd 206
 QY 61 FTLTMSVDRIYAVCHPYKALDFRTPRLKAKIINICIMWLLSSVGSISAIYVGGTKVREDVD 120
 Db 207 vlcslqfddeswvdlfmkicvtfafvpylilivcytlmllrlksvrlssgredk 266
 QY 121 VIECLQFPDDDYSWVDLFMKICVFIFAFVLPVLIIVCYTLMILRLKXVRLSSGREKD 180
 Db 267 nrlrttklrvlvaavfllcwtpihlflvealgstshstaissyficalgytnssln 326
 QY 181 NXLRRITRLVLYVAVFWCWPPIHIFLVEALGSTSHSTAALSSYFICIALGYTNSSLN 240
 Db 327 pvlvafidenkrcfridcfipkmergstrvrvntvqdpasmdygm-nkpy 380
 QY 241 PVLVAFIDENKRCFRIDCFIPKMERGSTSRVNVQDPAYVREIDGMANKPY 295

RESULT 6 #type complete
 ENTRY JC2434
 TITLE kappa opioid receptor - mouse
 ORGANISM #formal_name Mus musculus #common_name house mouse
 DATE 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 05-Apr-1995

ACCESSIONS JC2434
 JC2434
 #authors Nishi, M.; Takeshima, H.; Mori, M.; Nakagawara, K.; Takeuchi,
 T.
 #journal Biochem. Biophys. Res. Commun. (1994) 205:1353-1357
 #title Structure and chromosomal mapping of genes for the mouse
 kappa-opioid receptor and an opioid receptor homologue
 (MOR-C).
 #accession JC2434
 #molecule_type mRNA
 #residues 1-380 #label NIS

GENETICS #map_position 1A2-3
 #map_units 86/2; 204/1
 #keywords receptor
 SUMMARY #length 380 #molecular-weight 42630 #checksum 9705

Query Match 94.8%; Score 2114; DB 14; Length 380;
 Best Local Similarity 92.5%; Pred. No. 0.00e+00;
 Matches 273; Conservative 13; Mismatches 8; Indels 1; Gaps 1;

Db 87 ytkmktatniyifnlaladalavttttmpfgsavylnmswpgfvtckivtsidymmtsi 146
 QY 1 YTKMKTATNIYIFNLADALAVTTTTFPGSTVYLNMSWPGVLCIKIVISIDYNNMTSI 60
 Db 147 ftltmsvdyriavchpykaidfrtprlkakiniiciwilaasvgsaisaivlgtkvredvd 206
 QY 61 FTLTMSVDRIYAVCHPYKALDFRTPRLKAKIINICIMWLLSSVGSISAIYVGGTKVREDVD 120

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Db 207 vtecllqppddagawwdl fmkicvayfctvbylilivoytlmlrlksyrlisgrred 266
QY 121 vtecllqppdddyrswmdemkicvifpavivylilivoytlmlrlkkyrlisgrred 180
Db 267 nllrlrlkrlvlyvavflllcwtrpnhflilvealgsstshsaaissyfctalgytnsin 326
QY 181 xnlrllrlvlyvavflllcwtrpnhflilvealgsstshsaaissyfctalgytnsin 240
Db 327 pylvafldeikfrctfrcfplkkmwrgstvrvtvqdpasmrdvggm-nkpy 380
QY 241 pylvafldeikfrctfrcfplkkmwrgstvrvtvqdpasmrdvggm-nkpy 295

RESULT 7
ENTRY #type complete
TITLE mu oploid receptor - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 15-Oct-1996

ACCESSIONS
REFERENCE A57510; I48665; I49300
#authors Kaufman, D.L.; Keith Jr., D.E.; Anton, B.; Tian, J.; Magendzo, K.; Newman, D.; Tran, T.H.; Lee, D.S.; Wen, C.; Xia, Y.R.; Lustig, A.J.; Evans, C.J.
#journal J Biol. Chem. (1995) 270:15877-15883
#title Characterization of the murine mu oploid receptor gene.
#accession A57510
#status nucleic acid sequence not shown
#molecule_type mRNA
#residues 1-398 #label KAU
#cross-references GB:U19380

REFERENCE I48665
#authors Min, B.H.; Augustin, L.B.; Felsheim, R.F.; Fuchs, J.A.; Ioh, H.H.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:9081-9085
#title Genomic structure analysis of promoter sequence of a mouse mu oploid receptor gene.
#cross-references M01D:94377496
#accession I48665
#status translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-398 #label RES
#cross-references EMBL:U10561; NID:g555696; CDS_P1D:g565069

REFERENCE I49300
#authors Rossi, G.C.; Pan, Y.X.; Brown, G.P.; Pasternak, G.W.
#journal FEBS Lett. (1995) 369:192-196
#title Antisense mapping the MOR-1 oploid receptor: evidence for alternative splicing and a novel morphine-6 beta-glucuronide receptor.
#cross-references M01D:95377399
#accession I49300
#status nucleic acid sequence not shown; translation not shown; translated from GB/EMBL/DBJ

#molecule_type mRNA
#residues 1-398 #label RE2
#cross-references EMBL:U26915; NID:g1055230; CDS_P1D:g1055231

GENETICS
#introns 95/2: 213/1; 386/3
#note gene name MOR
KEYWORDS alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein
SUMMARY #length 398 #molecular_weight 44421 #checksum 8164

Query Match 68.4%; Score 1524; DB 14; Length 398;
Best Local Similarity 65.7%; Pred. No. 7,356-223;
Matches 190; Conservative 47; Mismatches 48; Indels 4; Gaps 4;

Db 96 ytkmktalnuyiflalaalatalstlbfqsvnylmgtwpgfnlckivlsldymnftsi 155
QY 1 ftkmktalnuyiflalaalatalstlbfqsvnylmgtwpgfnlckivlsldymnftsi 60
156 ftkmktalnuyiflalaalatalstlbfqsvnylmgtwpgfnlckivlsldymnftsi 214

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QY      61 FTLMMSVCDKXIVACHVYKALDRPFLKALINICQIMWLSSSVGSIAIVYGGTKRVEDV 120
Db      215 -idcclfsbptw-ywenllkicvffafimpyllitvcygmllilksvymllsgsked 272
QY      121 VIECCLOFPDDDDSWMDLPMKICVFIFAFVPLIITVCTTLMLEKXVRLSGSREXD 180
Db      273 rnlrctrmvllvavavivcwtpbshlyvllkalltppetftgvswhfcfajgtytscln 332
QY      181 XNMRIRTLVAVVAVVAVVCMVPHHITLVEALGSHSHSIALSSYFFICALGTYTNSLIN 240
Db      333 pvlafidcmfkrctfrcfictstestlegqsarlrqutrehpstantvd 381
QY      241 PILAFIDENKRCRDFCEPFLKMXMRKXSTSRNR-NTVQDPAYLREID 288

RESULT      8
ENTRY      S34593      #type complete
TITLE      mu opiate receptor - rat
ORGANISM   #format_name Rattus norvegicus #common_name Norway rat
DATE       10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change
ACCESSIONS S34593; A48799; I58154
REFERENCE   S34592
#authors   Fukuda, K.; Kato, S.; Mori, K.; Nishi, M.; Takeshima, H.
#journal   FEBS Lett. (1993) 327:311-314
#title     Primary structures and expression from cDNAs of rat oploid
           receptor delta- and mu-subtypes.
#accession S34593
           #molecule_type mRNA
           #residues 1-398 #label FUK
REFERENCE   A48799
#authors   Wang, J.
#journal   Proc. Natl. Acad. Sci. U.S.A. (1993) 90:10230-10234
#title     Mu opiate receptor: cDNA Cloning and expression.
#cross-references MIMD:94052137
#accession A48799
           #status preliminary; translated from GB/EMBL/DBJ
           #molecule_type mRNA
           #residues 1-398 #label WAN
           #cross-references GB:L20684; NID:9409149; CDS_PID:9409150
REFERENCE   I58154
#authors   Thompson, R.C.; Mansour, A.; Akil, H.; Watson, S.J.
#journal   Neuron (1993) 11:903-913
#title     Cloning and pharmacological characterization of a rat mu
           oploid receptor.
#cross-references MIMD:94059560
#accession I58154
           #status preliminary; translated from GB/EMBL/DBJ
           #molecule_type mRNA
           #residues 1-398 #label WHO
           #cross-references GB:L22455; NID:9437671; CDS_PID:9437672
GENETICS   #gene MUDRI
SUMMARY    #length 398 #molecular_weight 44494 #checksum 8595

Query Match      68.3%; Score 1522; DB 14; Length 398;
Best Local Similarity 66.1%; Pred. No. 1,58e-222;
Matches 191; Conservative 45; Mismatches 49; Indels 4; Gaps 4
QY      96 ytkmktatniy.finaladalatslpfgsvnylmgtvfgllkivisidyymftsi 155
Db      1 YRKMTATNIYIFNLADALVTTIMPOSYYLNMSPFGVCLKIVISIDYNNMFTSI 60
QY      156 fclctmsvdrylavchpykaldftprnaklvnvcnwllssaiqlpymfmatyyrg-s 214
Db      61 FTLMMSVCDKXIVACHVYKALDRPFLKALINICQIMWLSSSVGSIAIVYGGTKRVEDV 120
QY      215 -idcclfsbptw-ywenllkicvffafimpyllitvcygmllilksvymllsgsked 272
Db      121 VIECCLOFPDDDDSWMDLPMKICVFIFAFVPLIITVCTTLMLEKXVRLSGSREXD 180
QY      273 rnlrctrmvllvavavivcwtpbshlyvllkalltppetftgvswhfcfajgtytscln 332
Db      181 XNMRIRTLVAVVAVVAVVCMVPHHITLVEALGSHSHSIALSSYFFICALGTYTNSLIN 240
Db      333 pvlafidcmfkrctfrcfictstestlegqsarlrqutrehpstantvd 381
QY      241 PILAFIDENKRCRDFCEPFLKMXMRKXSTSRNR-NTVQDPAYLREID 288

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SUMMARY	#length 400	#molecular-weight 44779	#checksum 3741
Query Match	68.3%;	Score 1522;	DB 13; Length 400;
Best Local Similarity	67.1%;	Pred. No. 1.58e-222;	
Matches 188;	Conservative	43; Mismatches 46;	Indels 3; Gaps 3
Dd	98 ytkmkrtatniyifnialadatslfipgsvnylmgtvfgfllckivisidyymftst 157		
OY	1 YTKMKRTATNIYIFNIALDALADLTITMPQSYVLLNSWPFSDVLCKIVISIDYYNMFTSI 60		
Dd	158 fclctmsvdryiaavchpkakldfrprnaklilncwailssaiqlpwmatktyrgq-s 216		
OY	61 FFLTMMASVDRYIAVCHPKALDEFRRPLAKIINIICWILSSVGESALVLEGTVREDDV 120		
Dd	217 -idcfltsbptw-ywenllkicvfifdlmpvillitvcyglmilirksvmlsgsked 274		
OY	121 VLECCLOFPDDDSYWDMLFMKICVFIEFAFVLPVLIHCVTLMILRLKXVALSGSEKD 180		
Dd	275 nrlrlrtmlylvvvavfiwcvtgphilyllkalvltipettqtvswhfcialgytnscln 334		
OY	181 NURLRITLVLVVAVFVWCPTPIHFFILVPLALSTSHSTAALSSYFCIALGYTNSELN 240		
Dd	335 pviylafldcnfkrcfrefcfdpsnsiegnstrirgrndr 374		
OY	241 PLTYAFLDENFRKCRDFCFPLKXMXMERXSIRRYVOD 280		
RESULT 10			
ENTRY	S65693 #type complete		
TITLE	opioid receptor mu variant MOR1A - human		
ORGANISM	#formal_name Homo sapiens #common_name man		
DATE	12-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 26-Jul-1996		
ACCESSIONS	S65693; S51216		
REFERENCE	Bare, L.A.; Mansson, E.; Yang, D.		
#authors	submitted to the EMBL Data Library, July 1994		
#submission	Expression of two variants of the human mu opioid receptor		
#description	mRNA in SK-N-SH cells and human brain.		
#accession	S65693		
#molecule_type	mRNA		
#residues	1-392 ##label BAR		
#cross-references	EMBL:U12569		
REFERENCE	S51215		
#authors	Bare, L.A.; Mansson, E.; Yang, D.		
#journal	FEBS Lett. (1994) 354:213-216		
#title	Expression of two variants of the human mu opioid receptor mRNA in SK-N-SH cells and human brain.		
#accession	S51216		
#molecule_type	mRNA		
#residues	367-392 ##label BAW		
SUMMARY	#length 392	#molecular-weight 43939	#checksum 6977
Query Match	68.2%;	Score 1520;	DB 13; Length 392;
Best Local Similarity	67.1%;	Pred. NO. 3.38e-222;	
Matches 188;	Conservative	43; Mismatches 46;	Indels 3; Gaps 3;
Dd	98 ytkmkrtatniyifnialadatslfipgsvnylmgtvfgfllckivisidyymftst 157		
OY	1 YTKMKRTATNIYIFNIALDALADLTITMPQSYVLLNSWPFSDVLCKIVISIDYYNMFTSI 60		
Dd	158 fclctmsvdryiaavchpkakldfrprnaklilncwailssaiqlpwmatktyrgq-s 216		
OY	61 FFLTMMASVDRYIAVCHPKALDEFRRPLAKIINIICWILSSVGESALVLEGTVREDDV 120		
Dd	217 -idcfltsbptw-ywenllkicvfifdlmpvillitvcyglmilirksvmlsgsked 274		
OY	121 VLECCLOFPDDDSYWDMLFMKICVFIEFAFVLPVLIHCVTLMILRLKXVALSGSEKD 180		
Dd	275 nrlrlrtmlylvvvavfiwcvtgphilyllkalvltipettqtvswhfcialgytnscln 334		
OY	181 NURLRITLVLVVAVFVWCPTPIHFFILVPLALSTSHSTAALSSYFCIALGYTNSELN 240		

[illegible]

Query Match	Best Local Similarity	Matches	Score	DB	Length
67.5%;	65.7%;	190;	1505;	14;	398;
Pred. No. 1.03e-219;		45;			
Mismatches 50;		Indels 4;			Gaps 4;
<p>Cloning, characterization, and distribution of a mu-opioid receptor in rat brain.</p> <p>#cross-references M01D:94246380</p> <p>#accession I56504</p> <p>##status preliminary; translated from GB/EMBL/DBJ</p> <p>##molecule-type mRNA</p> <p>##residues 1-398 ##label RES</p> <p>##cross-references EMBL:U55424; NID:91017731; CDS_PID:91017732</p> <p>SUMMARY #length 398 #molecular-weight 44403 #checksum 8604</p>					
96 ytkmktatniyifnlaladalastlpfgsvnylmgtwpgtllckivisidyymftsi	155				
1 ytkmktatniyifnlaladalastlpfgsvnylmgtwpgtllckivisidyymftsi	60				
156 flctctmavdyiaavhpvkaldfftrpnaktivncwmlssagldpvmfmatktyqg-s	214				
61 fltlmavdyriaavhpvkaldfftrpnaktivncwmlssagldpvmfmatktyqg-s	120				
215 -idctlfshptw-ywenllkicvgaifaifmpvllitvcyglmlilksvrmllsgsked	272				
121 vtecclofpdddywmdlpmkicvfaifvpiavllitvcytlmlrlkxvrlilsgsrex	180				
273 nrlrricrmvlyvvaavivcwtprhlyvllkalltbtetfcvswfhcjalaytscn	332				
181 xnlerrirrlvlyvvaavivcwtprhlyvllkalltbtetfcvswfhcjalaytscn	240				
333 pvlafaidenkrircfrcfclptssleqgnstvyrgntrhpbstantvd	381				
241 pvlafaidenkrircfrcfclptssleqgnstvyrgntrhpbstantvd	288				
<p>delta opiate receptor - human</p> <p>#formal_name Homo sapiens #common_name man</p> <p>06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change</p> <p>06-Sep-1996</p> <p>ACCESSIONS I38657</p> <p>REFERENCE I38657</p> <p>##authors Simonin, F.; Befort, K.; Gaveriaux-Ruff, C.; Mathes, H.; Napepey, V.; Lannes, B.; Michelotti, G.; Kieffer, B.</p> <p>Mol. Pharmacol. (1994) 46:1015-1021</p> <p>The human delta-opioid receptor: genomic organization, cDNA cloning, functional expression, and distribution in human brain.</p> <p>#cross-references M01D:95107267</p> <p>#accession I38657</p> <p>##status preliminary; translated from GB/EMBL/DBJ</p> <p>##molecule-type mRNA</p> <p>##residues 1-372 ##label RES</p> <p>##cross-references EMBL:U10504; NID:9501144; CDS_PID:9501145</p> <p>SUMMARY #length 372 #molecular-weight 40368 #checksum 1688</p>					
Query Match	65.4%;	Score 1458;	DB 13;	Length 372;	
Best Local Similarity	69.2%;	Pred. No. 6.26e-212;			
Matches 180;	Conservative 43;	Mismatches 33;	Indels 4;	Gaps 4;	
<p>Cloning, characterization, and distribution of a mu-opioid receptor in rat brain.</p> <p>#cross-references M01D:94246380</p> <p>#accession I56504</p> <p>##status preliminary; translated from GB/EMBL/DBJ</p> <p>##molecule-type mRNA</p> <p>##residues 1-398 ##label RES</p> <p>##cross-references EMBL:U55424; NID:91017731; CDS_PID:91017732</p> <p>SUMMARY #length 398 #molecular-weight 44403 #checksum 8604</p>					
77 ytkmktatniyifnlaladalastlpfgsqakylmetwpgfclckavlsidyymftsi	136				
1 ytkmktatniyifnlaladalastlpfgsqakylmetwpgfclckavlsidyymftsi	60				
137 flctmavdyriaavhpvkaldfftrpnaktivncwmlssagldpvmfmatktyqg-s	195				
61 fltlmavdyriaavhpvkaldfftrpnaktivncwmlssagldpvmfmatktyqg-s	120				
196 vv-cmlqfispaw-ywdtvlkicvflfsvpdlitvcyglmlilksvrmllsgsked	253				
121 vtecclofpdddywmdlpmkicvfaifvpiavllitvcytlmlrlkxvrlilsgsrex	180				

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Db 254 rsrrtrmlyvvgafvvcwaphifvlyvltvldirdpvlvvaahlcialyanssl 313
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 181 XNKRIRIRLVVAVVAVVVCWPIHFILVHALGSTSHSTA-ALSSYFCIALGYINSSL 239
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 314 npvlyafldenfkrcfrqlc 333
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 240 NPILYAFDENFKRCFRDPC 259

RESULT 14
ENTRY S34592 #type complete
TITLE delta opioid receptor - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change
      06-Sep-1996
ACCESSIONS S34592; I56571
REFERENCE Fukuda, K.; Kato, S.; Mori, K.; Nishi, M.; Takeshima, H.
#authors #journal FEBS Lett. (1993) 327:311-314
#title Primary structures and expression from cDNAs of rat opioid
#accession S34592
#molecule_type mRNA
#residues 1-372 ##label FUK
REFERENCE Aboud, M.E.
#authors #journal J. Neurosci. Res. (1994) 27:714-719
#title Molecular cloning and expression of a rat delta opioid
#accession I56571
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-372 ##label RES
#cross-references EMBL:U00475; NID:9403488; CDS_PID:9514211
GENETICS
SUMMARY #gene dorl
      #length 372 #molecular-weight 40449 #checksum 2221
Query Match 65.1%; Score 1452; DB 14; Length 372;
      Best Local Similarity 68.8%; Pred. No. 6,16e-211;
      Matches 179; Conservative 44; Mismatches 33; Indels 4; Gaps 4;

Db 77 ykikratatyyifnlaadaltstlpfgsakylnetwpgfelckavlsidyymftsl 136
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Qy 1 YRKMTATNIYIFNLADALVTTMPFQSTVYIMNSMFGVLCIKIVISIDYNNFTSI 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 137 fcltmmsvdrylavchpvykaldfrfpakaklinicivlasvgvypimmarvtpqrdga- 195
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 FLTMMMSVDRYIAVCHPVAKALDFRFPKAKIINICIMLSSSVGSAIVLGGTKVREDVD 120
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 196 vv-cmlqfispew-yvdtvltkicvflfafvvpillltvcygmllrlsvrllsgsked 253
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 121 VIECLOPDDDYSWMDLFMKICVFIFAFVLPVLIIVCYTIMLRKKVRLSSREKD 180
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 254 rslrrtrmlyvvgafvvcwaphifvlyvltvldirdpvlvvaahlcialyanssl 313
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 181 XNKRIRIRLVVAVVAVVVCWPIHFILVHALGSTSHSTA-ALSSYFCIALGYINSSL 239
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 314 npvlyafldenfkrcfrqlc 333
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 240 NPILYAFDENFKRCFRDPC 259

RESULT 15
ENTRY B48227 #type complete
TITLE delta opioid receptor 1 - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 26-May-1994 #sequence_revision 26-May-1994 #text_change
      01-Dec-1995
ACCESSIONS B48227; S37807; A48685
REFERENCE Yasuda, K.; Raynor, K.; Kong, H.; Breder, C.D.; Takeda, J.;
      Reisine, T.; Bell, G.I.

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#journal Proc. Natl. Acad. Sci. U.S.A. (1993) 90:6736-6740
#title Cloning and functional comparison of kappa and delta opioid
#accession B48227
#status preliminary
#molecule_type mRNA
#residues 1-372 ##label YAS
#cross-references GB:L11064
REFERENCE S37807
#authors Kieffer, B.L.; Befort, K.; Gaveriaux-Ruff, C.; Hirth, C.G.
#submission submitted to the EMBL Data Library, February 1993
#accession S37807
#status preliminary
#molecule_type mRNA
#residues 1-372 ##label KIE
#cross-references EMBL:L06322
REFERENCE A48685
#authors Bzdega, T.; Chih, H.; Kim, H.; Jung, H.H.; Kozak, C.A.; Klee,
      W.A.
#journal Proc. Natl. Acad. Sci. U.S.A. (1993) 90:9305-9309
#title Regional expression and chromosomal localization of the delta
#accession A48685
#cross-references M01D:9402364
#status preliminary
#molecule_type mRNA
#residues 8-372 ##label BZD
#cross-references NCBI:138618; NCBI:138619
#experimental_source NG108-15 hybrid cells
#note sequence extracted from NCBI backbone
      brain; G protein-coupled receptor; glycoprotein;
      phosphoprotein; transmembrane protein
SUMMARY #length 372 #molecular-weight 40561 #checksum 3372
Query Match 65.0%; Score 1448; DB 14; Length 372;
      Best Local Similarity 68.8%; Pred. No. 2,83e-210;
      Matches 179; Conservative 44; Mismatches 33; Indels 4; Gaps 4;

Db 77 ykikratatyyifnlaadaltstlpfgsakylnetwpgfelckavlsidyymftsl 136
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 1 YRKMTATNIYIFNLADALVTTMPFQSTVYIMNSMFGVLCIKIVISIDYNNFTSI 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 137 fcltmmsvdrylavchpvykaldfrfpakaklinicivlasvgvypimmarvtpqrdga- 195
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 FLTMMMSVDRYIAVCHPVAKALDFRFPKAKIINICIMLSSSVGSAIVLGGTKVREDVD 120
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 196 vv-cmlqfispew-yvdtvltkicvflfafvvpillltvcygmllrlsvrllsgsked 253
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 121 VIECLOPDDDYSWMDLFMKICVFIFAFVLPVLIIVCYTIMLRKKVRLSSREKD 180
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 254 rslrrtrmlyvvgafvvcwaphifvlyvltvldirdpvlvvaahlcialyanssl 313
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 181 XNKRIRIRLVVAVVAVVVCWPIHFILVHALGSTSHSTA-ALSSYFCIALGYINSSL 239
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 314 npvlyafldenfkrcfrqlc 333
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 240 NPILYAFDENFKRCFRDPC 259

Search completed: Tue Aug 26 14:52:49 1997
Job time : 24 secs.

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1. 2. 3. 4. 5. 6.

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(TM)

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msrccl_pp      protein - protein database search, using Smith-Waterman algorithm
Run on:        Tue Aug 26 07:57:57 1997;      MsrcPar time 10.91 Seconds
Tabular output not generated.                  573.506 Million cell updates/sec

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Title:	>US-08-292-694A-12
Description:	(1-295) from US08292694A.pep
Percent Score:	2229
Sequence:	1 YTKKATNTNIYFNALADA.....NTVDDPAYIRFDGSMNNKRV 295

Scoring table: PAM 150
Gap 11

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%

Database:

swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

statistics: Mean 48.180; Variance 97.876; scale 0.492

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	2192	98.3	380	7	OPRK_HUMAN	KAPPA-TYPE OPIOID REC	0.00e+00
2	2157	96.8	380	7	OPRK_CAVPO	KAPPA-TYPE OPIOID REC	0.00e+00
3	2136	95.8	380	7	OPRK_MOUSE	KAPPA-TYPE OPIOID REC	0.00e+00
4	2132	95.5	380	7	OPRK_RAT	KAPPA-TYPE OPIOID REC	0.00e+00
5	1524	68.4	398	7	OPRM_MOUSE	MU-TYPE OPIOID RECEPT	1.85e-278
6	1522	68.3	398	7	OPRM_RAT	MU-TYPE OPIOID RECEPT	4.80e-278
7	1520	68.2	400	7	OPRM_HUMAN	MU-TYPE OPIOID RECEPT	1.25e-277
8	1458	65.4	372	7	OPRD_HUMAN	DELTA-TYPE OPIOID REC	8.72e-265
9	1452	65.1	372	7	OPRD_RAT	DELTA-TYPE OPIOID REC	1.52e-263
10	1448	65.0	372	7	OPRD_MOUSE	DELTA-TYPE OPIOID REC	1.02e-263
11	1345	60.3	367	7	OPRX_RAT	PROBABLE OPIOID RECEPT	2.01e-241
12	1343	60.3	367	7	OPRX_MOUSE	PROBABLE OPIOID RECEPT	5.20e-241
13	1331	59.7	370	7	OPRX_HUMAN	PROBABLE OPIOID RECEPT	1.56e-238
14	1319	59.2	370	7	OPRX_CAVPO	PROBABLE OPIOID RECEPT	4.67e-236
15	830	37.2	391	9	SSR1_MOUSE	SOMATOSTATIN RECEPTOR	4.46e-136
16	830	37.2	391	9	SSR1_HUMAN	SOMATOSTATIN RECEPTOR	4.46e-136
17	830	37.2	391	9	SSR1_RAT	SOMATOSTATIN RECEPTOR	4.46e-136
18	822	36.9	384	9	SSR4_HUMAN	SOMATOSTATIN RECEPTOR	1.84e-113
19	816	36.9	388	9	SSR4_MOUSE	SOMATOSTATIN RECEPTOR	2.99e-113
20	810	36.3	384	9	SSR4_RAT	SOMATOSTATIN RECEPTOR	4.84e-122
21	789	35.4	368	9	SSR2_BOVIN	SOMATOSTATIN RECEPTOR	8.25e-118
22	789	35.4	369	9	SSR2_PIG	SOMATOSTATIN RECEPTOR	8.25e-118

23	788	35.4	369	9	SSR2_RAT	SOA10ST01AIN RECEPTOR	1.31e-12
24	785	35.2	369	9	SSR2_MOUSE	SOA10ST01AIN RECEPTOR	5.26e-12
25	760	35.0	369	9	SSR2_HUMAN	SOA10ST01AIN RECEPTOR	3.46e-12
26	736	33.0	333	4	GPR8_HUMAN	PROBABLE G PROTEIN-CO	3.65e-11
27	683	30.6	418	9	SSR3_HUMAN	SOA10ST01AIN RECEPTOR	1.44e-10
28	676	30.3	363	9	SSR5_HUMAN	SOA10ST01AIN RECEPTOR	3.58e-10
29	668	30.0	363	9	SSR5_RAT	SOA10ST01AIN RECEPTOR	1.40e-10
30	661	29.7	328	4	GPR7_HUMAN	PROBABLE G PROTEIN-CO	3.46e-10
31	601	27.0	428	9	SSR3_RAT	SOA10ST01AIN RECEPTOR	2.70e-90
32	599	26.9	428	9	SSR3_MOUSE	SOA10ST01AIN RECEPTOR	6.70e-90
33	555	24.5	349	4	GALR_HUMAN	GALANTIN RECEPTOR (GAL	2.77e-79
34	466	22.3	355	2	CAR1_HUMAN	C-C CHEMOKINE RECEPTOR	9.81e-70
35	466	22.3	359	1	AG2R_CANPA	TYPE-1 ANGIOTENSIN II	9.81e-70
36	490	22.0	363	1	AG22_MOUSE	TYPE-2 ANGIOTENSIN II	1.43e-68
37	488	21.9	363	1	AGC2_HUMAN	TYPE-2 ANGIOTENSIN II	3.49e-68
38	486	21.8	359	1	AG2R_HUMAN	TYPE-1A ANGIOTENSIN I	8.50e-68
39	486	21.8	363	1	AG22_RAT	TYPE-2 ANGIOTENSIN II	8.50e-68
40	483	21.7	359	1	AG2R_PIG	TYPE-1 ANGIOTENSIN II	8.50e-68
41	481	21.6	359	1	AG2R_RABT	TYPE-1 ANGIOTENSIN II	7.89e-67
42	481	21.6	359	1	AG2S_RAT	TYPE-1B ANGIOTENSIN I	7.89e-67
43	476	21.4	359	1	AG2S_MOUSE	TYPE-1B ANGIOTENSIN I	7.30e-66
44	475	21.3	359	1	AG2R_MOUSE	TYPE-1B ANGIOTENSIN I	1.44e-65
45	475	21.3	359	1	AG2R_BOVIN	TYPE-1 ANGIOTENSIN II	1.44e-65

ALIGNMENTS

ID	RESULT	1	STANDARD;	PRT;	380 AA.
AC	OPRK HUMAN	P1145;			
DT	01-FEB-1995 (REL. 31, CREATED)				
DT	01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)				
DT	01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)				
DE	KAPPA-TYPE OPIOID RECEPTOR (KOR-1).				
GN	OPRK1 OR OPRK.				
OS	HOMO SAPIENS (HUMAN).				
OC	EUMETAZOA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	ETHERIA; PRIMATES.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-PLACENTA.				
RX	MEDLINE: 9438360.				
RA	MANSSON E., BARE U.A., YANG D.;				
RL	BIOCHEM. BIOPHYS. RES. COMMUN. 202:1431-1437(1994).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-PLACENTA.				
RX	MEDLINE: 95350200.				
RA	STIMONIN F., GAVERIADIS-ROFF C., BEFORT K., LANNES B., MICHELETTI G.,				
RL	MATEI M.-G., CHARON G., BLOCH B., KEEFER B.;				
RL	PROC. NATL. ACAD. SCI. U.S.A. 92:7006-7010(1995).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-BRAIN:				
RX	MEDLINE: 95174504.				
RA	ZHU J., CHEN C., XUE J.C., KUNAPULI S., DESIEL J.K., LIU-CHEN L.-Y.				
RL	LIFE SCI. 56:201-207(1995).				
CC	-1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM				
CC	ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR				
CC	FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF				
CC	AUTONOMIC AND ENDOCRINE FUNCTIONS.				
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.				
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
CC	EMBL: U17298; G596070. -;				
DR	EMBL: L37362; G722618; -;				
DR	PIR: JC2338; JC2338.				
DR	MIM: 165196; -;				
DR	PROSITE: PS00237; G-PROTEIN RECEPTOR.				
KW	G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;				
KW	PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.				
FT	DOMAIN	1	58		
FT	TRANSMEM	59	85		
					1 (POTENTIAL).

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FT DOMAIN 86 95 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 96 117 2 (POTENTIAL).
FT DOMAIN 118 132 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 133 154 3 (POTENTIAL).
FT TRANSMEM 155 173 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 174 196 4 (POTENTIAL).
FT TRANSMEM 197 222 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 223 247 5 (POTENTIAL).
FT TRANSMEM 248 275 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 276 299 6 (POTENTIAL).
FT TRANSMEM 300 311 7 (POTENTIAL).
FT TRANSMEM 312 333 7 (POTENTIAL).
FT TRANSMEM 334 380 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 380 425 BY SIMILARITY.
FT DISULFID 131 210 PALMITATE (POTENTIAL).
FT LIPID 345 345 PALMITATE (POTENTIAL).
FT CARBOHYD 25 25 POTENTIAL.
FT CARBOHYD 39 39 POTENTIAL.
FT CONFID 2 2 E -> D (IN REF. 2 AND 3).
SQ SEQUENCE 380 AA; 42659 MW; 1980629E CRC32;

Query Match 98.3%; Score 2192; DB 7; Length 380;
Best Local Similarity 97.6%; Pred. No. 0.00e+00;
Matches 288; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

Db 87 ytkmktatniyifnlaladalvtltmpfgstvylnmswpfgdvckivisldyymftsi 146
Qy 1 ytkmktatniyifnlaladalvtltmpfgstvylnmswpfgdvckivisldyymftsi 60

Db 147 ftlmmasvdyriavchpkaldftfpkakiiniciwllsssvgisaiavgktvredvd 206
Qy 61 ftlmmasvdyriavchpkaldftfpkakiiniciwllsssvgisaiavgktvredvd 120

Db 207 vleeslqfpdddysswdlfmkicvfaivpviilivcytlmrlrlksvrlisgsrekd 266
Qy 121 vleeslqfpdddysswdlfmkicvfaivpviilivcytlmrlrlksvrlisgsrekd 180

Db 267 nrlrrlttlvlyvavavfvcwtpihifllvealgstshstalsyfcialgynssln 326
Qy 181 nrlrrlttlvlyvavavfvcwtpihifllvealgstshstalsyfcialgynssln 240

Db 327 pllyafldentkrctfrcfplkmmersgtsrvnvtqdaylnvqgv-nkpy 380
Qy 241 pllyafldentkrctfrcfplkmmersgtsrvnvtqdaylnvqgv-nkpy 295

RESULT 2
ID OPKR_CAVPO STANDARD; PRT; 380 AA.
AC P41144;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE KAPPA-TYPE OPIOID RECEPTOR (KOR-1).
OS CAVIA PORCELLUS (GUINEA PIG).
OC EUTHERIA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HARTLEY; TISSUE=BRAIN;
RA MEDLINE: 94224625.
RA XIE G.X., MENG F., MANSOUR A., THOMPSON R.C., HOVERSTEN M.T.,
RA GOLDSTEIN A., WATSON S.J., AKIL H.;
RA PROC. NATL. ACAD. SCI. U.S.A. 91:3779-3783(1994).
CC -1- FUNCTION: INHIBITS NEUTRANSITTER RELEASE BY REDUCING CALCIUM
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
CC FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF
CC AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: U04092: G476107; -.
DR GCRDE: GCR.0991; -.
DR PROSITE: PS00257; G-PROTEIN RECEPTOR.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.

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FT DOMAIN 1 58 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 59 85 1 (POTENTIAL).
FT DOMAIN 86 95 2 (POTENTIAL).
FT TRANSMEM 96 117 2 (POTENTIAL).
FT TRANSMEM 118 132 3 (POTENTIAL).
FT TRANSMEM 133 154 3 (POTENTIAL).
FT TRANSMEM 155 173 4 (POTENTIAL).
FT TRANSMEM 174 196 4 (POTENTIAL).
FT TRANSMEM 197 222 5 (POTENTIAL).
FT TRANSMEM 223 247 5 (POTENTIAL).
FT TRANSMEM 248 275 6 (POTENTIAL).
FT TRANSMEM 276 299 6 (POTENTIAL).
FT TRANSMEM 300 311 7 (POTENTIAL).
FT TRANSMEM 312 333 7 (POTENTIAL).
FT TRANSMEM 334 380 7 (POTENTIAL).
FT TRANSMEM 380 425 BY SIMILARITY.
FT DISULFID 131 210 PALMITATE (POTENTIAL).
FT LIPID 345 345 PALMITATE (POTENTIAL).
FT CARBOHYD 25 25 POTENTIAL.
FT CARBOHYD 39 39 POTENTIAL.
SQ SEQUENCE 380 AA; 42736 MW; F9F34C4C CRC32;

Query Match 96.8%; Score 2157; DB 7; Length 380;
Best Local Similarity 94.6%; Pred. No. 0.00e+00;
Matches 279; Conservative 10; Mismatches 5; Indels 1; Gaps 1;

Db 87 ytkmktatniyifnlaladalvtltmpfgstvylnmswpfgdvckivisldyymftsi 146
Qy 1 ytkmktatniyifnlaladalvtltmpfgstvylnmswpfgdvckivisldyymftsi 60

Db 147 ftlmmasvdyriavchpkaldftfpkakiiniciwllsssvgisaiavgktvredvd 206
Qy 61 ftlmmasvdyriavchpkaldftfpkakiiniciwllsssvgisaiavgktvredvd 120

Db 207 vleeslqfpdddysswdlfmkicvfaivpviilivcytlmrlrlksvrlisgsrekd 266
Qy 121 vleeslqfpdddysswdlfmkicvfaivpviilivcytlmrlrlksvrlisgsrekd 180

Db 267 nrlrrlttlvlyvavavfvcwtpihifllvealgstshstalsyfcialgynssln 326
Qy 181 nrlrrlttlvlyvavavfvcwtpihifllvealgstshstalsyfcialgynssln 240

Db 327 pllyafldentkrctfrcfplkmmersgtsrvnvtqdaylnvqgv-nkpy 380
Qy 241 pllyafldentkrctfrcfplkmmersgtsrvnvtqdaylnvqgv-nkpy 295

RESULT 3
ID OPKR_MOUSE STANDARD; PRT; 380 AA.
AC P33534;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE KAPPA-TYPE OPIOID RECEPTOR (KOR-1) (MSI-1).
OS MUS MUSCULUS (MOUSE).
OC EUTHERIA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA MEDLINE: 93342064.
RA YASUDA K., RAYNOR K., KONG H., BREDER C.D., TAKEDA J., REISINE T.,
RA BELL G.I.;
RA PROC. NATL. ACAD. SCI. U.S.A. 90:6736-6740(1993).
CC [2]
CC SEQUENCE FROM N.A.
CC MEDLINE: 95100967.
CC NISHI M., TAKESHITA H., MORI M., NAKAGAWARA K.I., TAKEUCHI T.;
CC BIOCHEM. BIOPHYS. RES. COMMUN. 205:1353-1357(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95251663.
RA LIU H.C., LU S., AUGUSTIN L.B., FELSHRIM R.F., CHEN H.C.,
RA LOH H.H., WEI L.N.;

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RL BIOCHEM. BIOPHYS. RES. COMMUN. 209:639-647(1995).
 CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
 CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
 CC FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF
 CC AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC TISSUE SPECIFICITY: BRAIN (NEOCORTEX, HIPPOCAMPUS, AMYGDALA,
 CC MEDIAL HYPOTHALAMUS, LOCUS CERULEUS, AND PARABRACHIAL
 CC NUCLEUS).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: L11065; G348249; -
 DR EMBL: D31665; G808876; -
 DR EMBL: D31663; G808876; JOINED.
 DR EMBL: D31664; G808876; JOINED.
 DR EMBL: S77872; G998532; -
 DR EMBL: S77868; G998532; JOINED.
 DR EMBL: S77869; G998532; JOINED.
 DR PIR: A48227; A48227.
 DR GCRDB: GCR_0635; -
 DR PROSITE: PS00237; G-PROTEIN RECEPTOR.
 KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
 KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
 FT DOMAIN 1 58
 FT TRANSMEM 59 85
 FT DOMAIN 86 95
 FT TRANSMEM 96 117
 FT DOMAIN 118 132
 FT TRANSMEM 133 154
 FT DOMAIN 155 173
 FT TRANSMEM 174 196
 FT DOMAIN 197 222
 FT TRANSMEM 223 247
 FT DOMAIN 248 275
 FT TRANSMEM 276 299
 FT DOMAIN 300 311
 FT TRANSMEM 312 333
 FT DOMAIN 334 380
 FT DISULFD 131 210
 FT LIPID 345 345
 FT CARBOHYD 25 25
 FT CARBOHYD 39 39
 FT CONFLICT 211 211
 FT CONFLICT 231 231
 SQ SEQUENCE 380 AA; 42652 MW; C6F33212 CRC32;
 Query Match 95.8%; Score 2136; DB 7; Length 380;
 Best Local Similarity 92.9%; Pred. No. 0.0e+00;
 Matches 274; Conservative 13; Mismatches 7; Indels 1; Gaps 1;

DT 01-FEB-1994 (REL. 28, CREATED)
 DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE KAPPA-TYPE OPIOID RECEPTOR (KOR-1).
 GN KOR-D.
 OS RATTUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE; 94059008.
 RA CHEN Y., MESTER A., LIU J., YU L.;
 RL BIOCHEM. J. 295:625-628(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 93374033.
 RA MINAMI M., TOYA T., KATAO Y., MAEKAWA K., NAKAMURA S., ONOGI T.,
 RA KANEKO S., SATOH M.;
 RL FEBS LETT. 329:291-295(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
 RX MEDLINE; 94059009.
 RA LI S., ZHU J., CHEN C., CHEN Y.-W., DERTEL J.K., ASHBY B.,
 RA LIU-CHEN L.-Y.;
 RL BIOCHEM. J. 295:629-633(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
 RX MEDLINE; 94052210.
 RA MENG F., XIE G.-X., THOMPSON R.C., MANSOUR A., GOLDSTEIN A.,
 RA WATSON S.J., AKIL H.,
 RL PROC. NATL. ACAD. SCI. U.S.A. 90:9954-9958(1993).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN-WISTAR; TISSUE-BRAIN;
 RX MEDLINE; 93380575.
 RA NISHI M., TAKESHIMA H., FUKUDA K., KATO S., MORI K.;
 RL FEBS LETT. 330:77-80(1993).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY;
 RX MEDLINE; 95204422.
 RA YAKOVLEV A.G., KRUGER K.E., PADEN A.I.;
 RL J. BIOL. CHEM. 270:6421-6424(1995).
 CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
 CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
 CC FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF
 CC AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC TISSUE SPECIFICITY: BRAIN (NEOCORTEX, HIPPOCAMPUS, AMYGDALA,
 CC MEDIAL HYPOTHALAMUS, LOCUS CERULEUS, AND PARABRACHIAL
 CC NUCLEUS).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: L22001; G409237; -
 DR EMBL: D16829; G404116; -
 DR EMBL: L22536; G425189; -
 DR EMBL: U00442; G403487; -
 DR EMBL: D16534; G415810; -
 DR EMBL: U17995; G727260; -
 DR EMBL: U17995; G727260; JOINED.
 DR EMBL: U17994; G727260; JOINED.
 DR PIR: S36143; S36143.
 DR PIR: S38825; S38825.
 DR GCRDB: GCR_0635; -
 DR GCRDB: GCR_0724; -
 DR GCRDB: GCR_0724; -
 DR GCRDB: GCR_0804; -
 DR GCRDB: GCR_0804; -
 DR PROSITE: PS00237; G-PROTEIN RECEPTOR.
 KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
 KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
 FT DOMAIN 1 58
 FT TRANSMEM 59 85
 FT DOMAIN 86 95
 FT TRANSMEM 96 117

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FT DOMAIN 118 132 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 133 154 3 (POTENTIAL).
FT DOMAIN 154 173 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 174 196 4 (POTENTIAL).
FT TRANSMEM 197 222 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 223 247 5 (POTENTIAL).
FT TRANSMEM 248 275 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 276 299 6 (POTENTIAL).
FT TRANSMEM 300 311 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 312 333 7 (POTENTIAL).
FT TRANSMEM 334 380 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 380 421 7 (POTENTIAL).
FT TRANSMEM 421 441 7 (POTENTIAL).
FT TRANSMEM 441 461 7 (POTENTIAL).
FT TRANSMEM 461 481 7 (POTENTIAL).
FT TRANSMEM 481 501 7 (POTENTIAL).
FT TRANSMEM 501 521 7 (POTENTIAL).
FT TRANSMEM 521 541 7 (POTENTIAL).
FT TRANSMEM 541 561 7 (POTENTIAL).
FT TRANSMEM 561 581 7 (POTENTIAL).
FT TRANSMEM 581 601 7 (POTENTIAL).
FT TRANSMEM 601 621 7 (POTENTIAL).
FT TRANSMEM 621 641 7 (POTENTIAL).
FT TRANSMEM 641 661 7 (POTENTIAL).
FT TRANSMEM 661 681 7 (POTENTIAL).
FT TRANSMEM 681 701 7 (POTENTIAL).
FT TRANSMEM 701 721 7 (POTENTIAL).
FT TRANSMEM 721 741 7 (POTENTIAL).
FT TRANSMEM 741 761 7 (POTENTIAL).
FT TRANSMEM 761 781 7 (POTENTIAL).
FT TRANSMEM 781 801 7 (POTENTIAL).
FT TRANSMEM 801 821 7 (POTENTIAL).
FT TRANSMEM 821 841 7 (POTENTIAL).
FT TRANSMEM 841 861 7 (POTENTIAL).
FT TRANSMEM 861 881 7 (POTENTIAL).
FT TRANSMEM 881 901 7 (POTENTIAL).
FT TRANSMEM 901 921 7 (POTENTIAL).
FT TRANSMEM 921 941 7 (POTENTIAL).
FT TRANSMEM 941 961 7 (POTENTIAL).
FT TRANSMEM 961 981 7 (POTENTIAL).
FT TRANSMEM 981 1000 7 (POTENTIAL).

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DR EMBL: U10558; G565069; JOINED.
DR EMBL: U10559; G565068; JOINED.
DR EMBL: U10560; G565069; JOINED.
DR EMBL: U26915; G1055231; -.
DR PROSITE: PS00237; G-PROTEIN-RECEPTOR.
DR G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT TRANSMEM 1 64 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 65 94 1 (POTENTIAL).
FT TRANSMEM 95 103 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 104 121 2 (POTENTIAL).
FT TRANSMEM 122 143 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 144 163 3 (POTENTIAL).
FT TRANSMEM 164 193 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 194 209 4 (POTENTIAL).
FT TRANSMEM 210 234 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 235 257 5 (POTENTIAL).
FT TRANSMEM 258 280 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 281 303 6 (POTENTIAL).
FT TRANSMEM 304 311 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 312 328 7 (POTENTIAL).
FT TRANSMEM 329 398 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 398 421 7 (POTENTIAL).
FT TRANSMEM 421 441 7 (POTENTIAL).
FT TRANSMEM 441 461 7 (POTENTIAL).
FT TRANSMEM 461 481 7 (POTENTIAL).
FT TRANSMEM 481 501 7 (POTENTIAL).
FT TRANSMEM 501 521 7 (POTENTIAL).
FT TRANSMEM 521 541 7 (POTENTIAL).
FT TRANSMEM 541 561 7 (POTENTIAL).
FT TRANSMEM 561 581 7 (POTENTIAL).
FT TRANSMEM 581 601 7 (POTENTIAL).
FT TRANSMEM 601 621 7 (POTENTIAL).
FT TRANSMEM 621 641 7 (POTENTIAL).
FT TRANSMEM 641 661 7 (POTENTIAL).
FT TRANSMEM 661 681 7 (POTENTIAL).
FT TRANSMEM 681 701 7 (POTENTIAL).
FT TRANSMEM 701 721 7 (POTENTIAL).
FT TRANSMEM 721 741 7 (POTENTIAL).
FT TRANSMEM 741 761 7 (POTENTIAL).
FT TRANSMEM 761 781 7 (POTENTIAL).
FT TRANSMEM 781 801 7 (POTENTIAL).
FT TRANSMEM 801 821 7 (POTENTIAL).
FT TRANSMEM 821 841 7 (POTENTIAL).
FT TRANSMEM 841 861 7 (POTENTIAL).
FT TRANSMEM 861 881 7 (POTENTIAL).
FT TRANSMEM 881 901 7 (POTENTIAL).
FT TRANSMEM 901 921 7 (POTENTIAL).
FT TRANSMEM 921 941 7 (POTENTIAL).
FT TRANSMEM 941 961 7 (POTENTIAL).
FT TRANSMEM 961 981 7 (POTENTIAL).
FT TRANSMEM 981 1000 7 (POTENTIAL).

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R2  SEQUENCE FROM N.A.
RC  TISSUE-BRAIN;
RX  MEDLINE; 94052137.
RA  WANG J.-B., IMAT Y., EPLER M.C., GREGOR P., SPIVAK C., UHL G.R.;
RL  PROC. NATL. ACADE. SCI. U.S.A. 90:10230-10234(1993).
RN  [3]
R2  SEQUENCE FROM N.A.
RC  TISSUE-BRAIN;
RX  MEDLINE; 93341493.
RA  CHEN Y., MESTER A., LUT J., HURLEY J.A., YU L.;
RL  MOL. PHARMACOL. 44:8-12(1993).
RN  [4]
R2  SEQUENCE FROM N.A.
RC  STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
RA  BONZOM J.R., GRANDY D.K., KELLY M.;
RL  SUBMITTED (SEP-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
RN  [5]
R2  SEQUENCE FROM N.A.
RC  STRAIN-SPRAGUE-DAWLEY; TISSUE-OLFACTORY BULB;
RX  MEDLINE; 94059560.
RA  THOMPSON R.C., MANSOUR A., AKIL H., WATSON S.J.;
RL  NEURON 11:903-913(1993).
RN  [6]
CC  -I- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC  ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
CC  FOR BETA-ENDOPHIN.
CC  -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC  -I- TISSUE SPECIFICITY: BRAIN, WITH HIGH CONCENTRATIONS IN THE
CC  BRAINSTEM AND CEREBRUM. NOT DETECTED IN CEREBELLUM.
CC  -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR  EMBL; L20684; G409150; -
DR  EMBL; L13069; G348251; -
DR  EMBL; U02083; G403574; -
DR  EMBL; L22455; G437672; -
DR  PIR; S34593; S34593.
DR  GCRDB; GCR_0633; -
DR  GCRDB; GCR_0637; -
DR  GCRDB; GCR_0639; -
DR  GCRDB; GCR_0640; -
DR  GCRDB; GCR_0644; -
DR  PROSITE; PS00237; G_PROTEIN_RECEPTOR.
KW  G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW  PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT  DOMAIN 1 64
FT  TRANSMEM 94
FT  DOMAIN 95 103
FT  TRANSMEM 104 121
FT  DOMAIN 122 143
FT  TRANSMEM 144 163
FT  DOMAIN 164 193
FT  TRANSMEM 194 209
FT  DOMAIN 210 234
FT  TRANSMEM 235 257
FT  DOMAIN 258 280
FT  TRANSMEM 281 303
FT  DOMAIN 304 311
FT  TRANSMEM 312 328
FT  DOMAIN 329 398
FT  DISULFID 140 217
FT  LIPID 351 351
FT  CARBOHYD 9 9
FT  CARBOHYD 31 31
FT  CARBOHYD 38 38
FT  CARBOHYD 46 46
FT  CARBOHYD 53 53
FT  CONFLICT 245 245
SQ  SEQUENCE 398 AA; 44494 MW; 2C21013D CRC32;

Query Match 68.3%; Score 1522; DB 7; Length 398;
Best Local Similarity 66.1%; Pred. No. 4,80e-278;
Matches 191; Conservative 45; Mismatches 49; Indels 4; Gaps 4;
Db 96 ytkmktatniyifnlaladalaistlplfgsvnyimgtwpflltcklvlsldgymtstl 155

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QY 1 YTKMKTATNIYIFNLALADALAVTTMPFQSTVYLMNSWMPFGVDLCKVISTDIYNMFTSI 60
Db 156 ftlctmsvdyiavchvkaldfcpnakiwvncwllsaisglpymfmatekyrgs- 214
QY 61 flltmsvdyriavchvkaldfcpnakiwvncwllsaisglpymfmatekyrgs- 120
Db 215 -idctlfshptw-ywenllkicvffafimpyllilevgylmllrksvrmjsgsked 272
QY 121 VIEGCLQFPDDDSWMDLFKICVFIFAEVPIVLIIVCYTLMILRLKXVRLLSGSRKED 180
Db 273 nrlrllrmwlvvavayfiwcpvhlhyllkaltipettfgvshfclagytscln 332
QY 181 XNRRIRRLVAVVAVFVQWMTIHIFILVEALGISHSLAALSSIFCYALGYNSSLN 240
Db 333 pylvafidenkfcrcfcicpisttlegqnsrtvrgutrehstantvd 381
QY 241 PILYAFIDENFKRCFDFCPFLKMXMERKXSTSHVR-NYQDPAYLKEID 268

RESULT 7
ID OPRM.HUMAN STANDARD; PRT; 400 AA.
AC P35372;
DT 01-JUN-1994 (REL. 29, CREATED)
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE MU-TYPE OPTOID RECEPTOR (MOR-1).
GN OPRM1 OR MOR1.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE; 94139928.
RA WANG J.-B., JOHNSON P.S., PERSICO A.M., HAWKINS A.L., GRIFFIN C.A.,
RA UHL G.R.;
RL FEBS LETT. 338:217-222(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA MESTER A. JR., HURLEY J.H., BYE L.S., CAMPBELL A., TIAN M.,
RA CHEN Y., YU L.;
RL SUBMITTED (XXX-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -I- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
CC FOR BETA-ENDOPHIN.
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR  EMBL; L25119; G452073; -
DR  EMBL; L29301; G459832; -
DR  GCRDB; GCR_0685; -
DR  GCRDB; GCR_0966; -
DR  MIM; 600018; -
DR  PROSITE; PS00237; G_PROTEIN_RECEPTOR.
KW  G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW  PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT  DOMAIN 1 66
FT  TRANSMEM 67 96
FT  DOMAIN 97 105
FT  TRANSMEM 106 123
FT  DOMAIN 124 145
FT  TRANSMEM 146 165
FT  DOMAIN 166 195
FT  TRANSMEM 196 211
FT  DOMAIN 212 236
FT  TRANSMEM 237 259
FT  DOMAIN 260 282
FT  TRANSMEM 283 305
FT  DOMAIN 306 313
FT  TRANSMEM 314 330
FT  DOMAIN 331 400
FT  DISULFID 142 219

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FT LIPID 353 353 PALMITATE (POTENTIAL).
 FT CARBOHYD 9 9 POTENTIAL.
 FT CARBOHYD 12 12 POTENTIAL.
 FT CARBOHYD 33 33 POTENTIAL.
 FT CARBOHYD 40 40 POTENTIAL.
 FT CARBOHYD 48 48 POTENTIAL.
 FT CONFLICT 51 51 N -> D (IN REF. 2).
 FT CONFLICT 234 234 V -> L (IN REF. 2).
 SQ SEQUENCE 400 AA; 44764 MW; 3F40D610 CRC32;
 Query Match 68.2%; Score 1520; DB 7; Length 400;
 Best Local Similarity 67.1%; Pred. No. 1.25e-277;
 Matches 188; Conservative 43; Mismatches 46; Indels 3; Gaps 3;
 Db 98 ytkmktanififnlaladalastlbfgsakymtwpfgtlckaylsidyyumfts1 157
 1 ytkmktanififnlaladalastlbfgsakymtwpfgtlckaylsidyyumfts1 60
 Db 158 ftltmsvdyriavchpykaldfrtpakaklinciwlaagvyvplmavtrpda- 216
 61 ftltmsvdyriavchpykaldfrtpakaklinciwlaagvyvplmavtrpda- 120
 Db 217 -idctltshptw-ywelnvkvicvflafvplvllitvcygmllrlksvmlsgsked 274
 121 vtecltppdddyvswdldfkmkicvflafvplvllitvcygmllrlksvmlsgsked 180
 Db 275 nrlritmvlvvaavfvcwcpnlhfvwllvlgldrrdpjvaalhalcylgyanss1 334
 181 nrlritmvlvvaavfvcwcpnlhfvwllvlgldrrdpjvaalhalcylgyanss1 240
 Db 335 pylyafldenfkrcifrcfciptsniequnstrinqtrd 374
 241 ptylyafldenfkrcifrcfciptsniequnstrinqtrd 280
 QY
 Db 335 pylyafldenfkrcifrcfciptsniequnstrinqtrd 374
 241 ptylyafldenfkrcifrcfciptsniequnstrinqtrd 280
 QY
 RESULT 8
 ID OPD_HUMAN STANDARD; PRT; 372 AA.
 AC P41143;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE DELTA-TYPE OPIOID RECEPTOR (DOR-1).
 GN OPRD1 OR OPRD.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 CC [1]
 RN RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=CEREBRAL CORTEX, AND STRIATUM;
 RX MEDLINE; 94260835.
 RA KANAP R.J., MALATYNSKA E., FANG L., LI X., BABIN E., NGUYEN M.,
 RA SANCRO G., VARGA E.Y., HRUBY V.J., ROESKE W.R., YAMAMURA H.I.;
 RL LIFE SCI. 54:463-469(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 95107267.
 RA SIMONIN F., BEFORT K., GAVERIAUX-ROFF C., MATTHES H., NAPPET V.,
 RA LANNES B., MICHELETI G., KIEFFER B.;
 RL MOL. PHARMACOL. 46:1015-1021(1994).
 CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
 ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. HIGHLY
 STEREOSELECTIVE. RECEPTOR FOR ENKEPHALINS.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; 070862; G497314; -
 DR EMBL; 010504; E162517; -
 DR MIM; 165195; -
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR.
 KM G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
 PHOSPHORYLATION; LIPOPROTEIN; EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 1 45
 FT TRANSMEM 46 75
 FT DOMAIN 76 84
 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 85 102
 FT DOMAIN 103 124
 FT TRANSMEM 125 144
 FT TRANSMEM 145 174
 FT TRANSMEM 175 190
 FT TRANSMEM 191 215
 FT TRANSMEM 216 238
 FT TRANSMEM 239 261
 FT TRANSMEM 262 284
 FT TRANSMEM 285 293
 FT TRANSMEM 294 310
 FT TRANSMEM 311 372
 FT TRANSMEM 318 372
 FT CARBOHYD 33 33
 FT CARBOHYD 121 198
 FT LIPID 333 333
 FT CONFLICT 27 27
 FT CONFLICT 40 41
 FT CONFLICT 348 348
 FT CONFLICT 370 370
 SQ SEQUENCE 372 AA; 40450 MW; CFF92985 CRC32;
 Query Match 65.4%; Score 1458; DB 7; Length 372;
 Best Local Similarity 69.2%; Pred. No. 8.72e-265;
 Matches 180; Conservative 43; Mismatches 33; Indels 4; Gaps 4;
 Db 77 ytkmktanififnlaladalastlbfgsakymtwpfgtlckaylsidyyumfts1 136
 1 ytkmktanififnlaladalastlbfgsakymtwpfgtlckaylsidyyumfts1 60
 QY
 Db 137 ftltmsvdyriavchpykaldfrtpakaklinciwlaagvyvplmavtrpda- 195
 61 ftltmsvdyriavchpykaldfrtpakaklinciwlaagvyvplmavtrpda- 120
 QY
 Db 196 vv-cmlqfpspw-ywdtvekvicvflafvplvllitvcygmllrlksvmlsgsked 253
 121 vtecltppdddyvswdldfkmkicvflafvplvllitvcygmllrlksvmlsgsked 180
 Db 254 rslritmvlvvaavfvcwcpnlhfvwllvlgldrrdpjvaalhalcylgyanss1 313
 181 nrlritmvlvvaavfvcwcpnlhfvwllvlgldrrdpjvaalhalcylgyanss1 239
 QY
 Db 314 nplyafldenfkrcifrcfciptsniequnstrinqtrd 374
 240 nplyafldenfkrcifrcfciptsniequnstrinqtrd 259
 QY
 RESULT 9
 ID OPD_RAT STANDARD; PRT; 372 AA.
 AC P33533;
 DT 01-FEB-1994 (REL. 28, CREATED)
 DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE DELTA-TYPE OPIOID RECEPTOR (DOR-1) (OPIOID RECEPTOR A).
 GN ROR-A.
 OS RATTUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 CC [1]
 RN RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RX MEDLINE; 93351652.
 RA FUKUDA K., KATO S., MORI K., NISHI M., TAKESHIMA H.;
 RL FEBS LETT. 327:311-314(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
 RX MEDLINE; 94322412.
 RA ABOOD M.E., NOEL M.A., FARNSWORTH J.S., TAO Q.;
 RL J. NEUROSCI. RES. 37:714-719(1994).
 CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
 ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. HIGHLY
 STEREOSELECTIVE. RECEPTOR FOR ENKEPHALINS.

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CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: D16348; G391865; -.
DR EMBL: D00475; G514211; -.
DR PIR: S34592; S34592.
DR GCRDB: GCR_0638; -.
DR GCRDB: GCR_0805; -.
DR PROSITE: PS00237; G-PROTEIN RECEPTOR.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
FM PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 45
FT TRANSMEM 46 75
FT DOMAIN 76 84
FT TRANSMEM 85 102
FT DOMAIN 103 124
FT TRANSMEM 125 144
FT DOMAIN 145 174
FT TRANSMEM 175 190
FT DOMAIN 191 215
FT TRANSMEM 216 238
FT DOMAIN 239 261
FT TRANSMEM 262 284
FT DOMAIN 285 293
FT TRANSMEM 294 310
FT DOMAIN 311 372
FT CARBOHYD 18 18
FT CARBOHYD 33 33
FT DISULFID 121 198
FT LIPID 333 333
SQ SEQUENCE 372 AA; 40449 MW; 59F5E50 CRC32;

Query Match 65.1%; Score 1452; DB 7; Length 372;
Best Local Similarity 68.8%; Pred. No. 1.02e-262;
Matches 179; Conservative 44; Mismatches 33; Indels 4; Gaps 4;

DQ 77 ytklktatniyifnlaladalstclpfgeakymetwpgfllckavlsldymnfstsi 136
QY 1 ytkmktatniyifnlaladalstclpfgeakymetwpgfllckavlsldymnfstsi 60
DQ 137 ftltmmsvdyrlavchpkykaldftrpakaklnicwvlasvgyplmvmavtqprdga- 195
QY 61 ftltmmsvdyrlavchpkykaldftrpakaklnicwvlasvgyplmvmavtqprdga- 120
DQ 196 vv-cltqlgfpdsw-ywtdvckicvflfaivpvlitvcygmllflsvylslsskckd 253
QY 121 vlecclapdddywmwclcmkicvflfaivpvlitvcygmllflsvylslsskckd 180
DQ 254 tsllritcmvllvvvgafvvcwapihlfivwclvdiinrcdljvaalhlclalgyanssl 313
QY 181 xnlrkitrlvlyvvaavfvcwtpfihflvwalgststshsta-alsstyfclalgttnssl 239
DQ 314 npvlyafldetkfcfcfgdc 333
QY 240 npliafldenfkrcfndfc 259

RESULT 10
ID OPER. MOUSE STANDARD; PRT: 372 AA.
AC P32300;
DT 01-OCT-1993 (REL. 27, CREATED)
DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE DELTA-TYPE OPIOID RECEPTOR (DOR-1) (K56) (MSL-2).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 93101664.
RA KIEFER B.L., BEFORT K., GAVERIAUX-RUFF C., HIRSH C.G.;
RL PROC. NATL. ACAD. SCI. U.S.A. 89:12048-12052(1992).
RN [2]
SQ SEQUENCE FROM N.A.

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RX MEDLINE: 93101664.
RA EVANS C.J., KEITH D.E. JR., MORRISON H., MAGENDZO K., EDWARDS R.H.;
RL SCIENCE 258:1952-1955(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE: 93342064.
RA YASUDA K., RAYNOR K., KONG H., BREDER C.D., TAKEDA J., REISINE T.,
RA BELL G.I.;
RL PROC. NATL. ACAD. SCI. U.S.A. 90:6736-6740(1993).
RN [4]
RP SEQUENCE FROM N.A.
RA KEITH D.E. JR., ANTON B., EVANS C.J.;
RL PROC. WEST. PHARMACOL. SOC. 36:299-306(1993).
RN [5]
RP SEQUENCE OF 8-372 FROM N.A.
RX MEDLINE: 94022364.
RA BZDEGA T., CHIN H., KIM K., JUNG H.H., KOZAK C.A., KLEE W.A.;
RL PROC. NATL. ACAD. SCI. U.S.A. 90:9305-9309(1993).
RN [6]
RP 3D-STRUCTURE MODELLING.
RX MEDLINE: 97001837.
RA ALKORTA I., LOEW G.H.;
RL PROTEIN ENG. 9:573-583(1996).
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. HIGHLY
STERESELECTIVE. RECEPTOR FOR ENKEPHALINS.
CC -1- TISSUE SPECIFICITY: BRAIN, WITH HIGH CONCENTRATIONS IN THE BASAL
GANGLIA AND LIMBIC REGIONS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: L06322; G192943; -.
DR EMBL: L07271; -. NOT ANNOTATED_CDS.
DR EMBL: L11064; G348247; -.
DR EMBL: S65335; G442326; -.
DR EMBL: S66181; G435782; -.
DR PIR: S37807; S37807.
DR PIR: B48227; B48227.
DR GCRDB: GCR_0229; -.
DR GCRDB: GCR_0493; -.
DR GCRDB: GCR_0634; -.
DR GCRDB: GCR_0634; -.
DR GCRDB: GCR_0642; -.
DR GCRDB: GCR_0822; -.
KW G-PROTEIN COUPLED RECEPTOR.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
FM PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 45
FT TRANSMEM 46 75
FT DOMAIN 76 84
FT TRANSMEM 85 102
FT DOMAIN 103 124
FT TRANSMEM 125 144
FT DOMAIN 145 174
FT TRANSMEM 175 190
FT DOMAIN 191 215
FT TRANSMEM 216 238
FT TRANSMEM 239 261
FT TRANSMEM 262 284
FT DOMAIN 285 293
FT TRANSMEM 294 310
FT DOMAIN 311 372
FT CARBOHYD 18 18
FT CARBOHYD 33 33
FT DISULFID 121 198
FT LIPID 333 333
SQ SEQUENCE 372 AA; 40561 MW; 514022P5 CRC32;

Query Match 65.0%; Score 1448; DB 7; Length 372;
Best Local Similarity 68.8%; Pred. No. 1.02e-262;
Matches 179; Conservative 44; Mismatches 33; Indels 4; Gaps 4;

DQ 77 ytklktatniyifnlaladalstclpfgeakymetwpgfllckavlsldymnfstsi 136
QY 1 ytkmktatniyifnlaladalstclpfgeakymetwpgfllckavlsldymnfstsi 60

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QY	2	TRYKATANNITYIENMLADALVTTMTDFQOSVYLMNMSWPEGDVLCIKIVISIDYYNMTSIF	61
Db	137	tlitamsvdyryvaachpirladvtstskadavnaivalasvgyvpaalmgsqgv-ede-	194
QY	62	TLTMSASVDRIATVCHVKALDEFPTPLAKATINICIMLSSSVGISAIIVGGKRVEDDV	121
Db	195	leclveipadpqd-wgvpfa-icifsfstipylisvcsymtirrlgvrlllsgsrek	252
QY	122	IECLOQEPD-DPXSMDWDLFMKICVFEAFVAVIPVLLIIVCITMLIRLKKYRLLSGSREK	180
Db	253	rlrlrlrlrlrlvrvavayfvgcwrvpyfvylvgq]vgvpsgetavallrfctalgynscn	312
QY	181	XNLRRIITRLVVAAYVAVVOCWPIHIFILVEALGSISHSTALSSYFICIALGYINSSLN	240
Db	313	pilyafidenfkacffkfoacaalhemqsdavtsiad	352
QY	241	PLIYAFIDENFKCFERDFCFPLKMXKXSTSRVNTVQD	280
RESULT	13	STANDARD:	PRT: 370 AA.
ID	OPRX_HUMAN	STANDARD:	PRT: 370 AA.
AC	P41146:		
DT	01-FEB-1995 (REL. 31, CREATED)		
DT	01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)		
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)		
DE	PROBABLE	476	POTENTIAL.
FT	CARBOHYD	532	POTENTIAL.
FT	CARBOHYD	540	POTENTIAL.
FT	CARBOHYD	556	POTENTIAL.
FT	CARBOHYD	576	POTENTIAL.
FT	CARBOHYD	623	POTENTIAL.
FT	CARBOHYD	645	POTENTIAL.
FT	CARBOHYD	2041	POTENTIAL.
FT	CARBOHYD	2077	POTENTIAL.
FT	CARBOHYD	2240	POTENTIAL.
FT	CARBOHYD	2364	POTENTIAL.
FT	CARBOHYD	2789	POTENTIAL.
SQ	SEQUENCE	3011 AA; 327197 MW; 0768B84 CRC32;	
Query Match		95.7%; Score 4322; DB 7; Length 3011;	
Best Local Similarity		92.7%; Pred. No. 0.00e+00;	
Matches	585; Conservative	35; Mismatches 11; Indels 0; Gaps 0;	
Db	1027	aplitayagqtgcllsciltsltyrdkqvegeevq]vstaaqtlfctcngvcwtvynag	1086
QY	1	APITAYSQTRGLLACITTSLGSDKKNBESEVYSTATQSFLATCVNGVCWTVYHGAG	60
Db	1087	trtlaspkpyv]qmytnvdqqlvgwppaggrsrltpccgsadllyltnhadviprrng	1146
QY	61	SKTLIAPKGPITQWNTVNDQDVGMPKPKPGRKSLTPTCCSSDLIYTRHADVIVARRG	120
Db	1147	dsrsgllpprpisylksgsggpllpaghavq]frinaovctryakavd]ipven]etmr	1206
QY	121	DSRGSLLPPRVSYLKSGSGGPLLCPRGHAQV]FRAVCTRGVAKADVPESMETMR	180
Db	1207	spvfcdnssppvqgsf]vahlhaptsgystkpraaayaggykv]vlnpsvaact]gfga	1266
QY	181	SPVFTDNSSPFAVQOSQVAHLHAPTSQGSTKVPAAVIAAGYKV]VLPNSVAATIGFGA	240
Db	1267	ymskahgldpnlrtgvtcltsgpsltsytkg]fadqsgcsgayvdi]ldechstatel	1326
QY	241	YMSKAHGIDPNIIRGCVMTITTGAVYVSTYTKGLADOGCGGAYDI]LICECHSTDSYTI	300
Db	1327	lgistvt]dqgaetagar]vlatatppgsvtvp]bnleevalst]tgelpfygaalp]evlx	1386
QY	301	LGISTVTDQOETAGAR]VYLATATPPGSVTVPPBNIEEVALNSTGELPFYGNALP]EALR	360
Db	1387	ggrll]fchakkkcdelaak]lvalg]lnavayyq]d]sv]lps]sgdvvvvataclmtytg	1446
QY	361	GGRLLIFCHSKKKCDELAALSGG]LNAVAYYQ]D]SV]LPGDVVAVVATDAM]GYTG	420
Db	1447	d]d]sv]lps]sgdvvvvataclmtytg	1506

	Query Match	94.5%;	Score 4266;	DB 7;	Length 3011;
	Best Local Similarity	91.9%;	Pred. No. 0.0e+00;		
	Matches 580;	Conservative	38;	Mismatches 13;	Indels 0; Caps 0;
FT	CARBOHYD	5/6	5/6	POTENTIAL.	
FT	CARBOHYD	623	623	POTENTIAL.	
FT	CARBOHYD	645	645	POTENTIAL.	
FT	CARBOHYD	2041	2041	POTENTIAL.	
FT	CARBOHYD	2240	2240	POTENTIAL.	
FT	CARBOHYD	2364	2364	POTENTIAL.	
FT	CARBOHYD	2789	2789	POTENTIAL.	
SO	SEQUENCE	3011 AA;	327142 MW;	49643481 CPG32;	
Db	1087	trfaspkxpriqytwddgdlvwpapagsrsitpctcgssdlylvtbnadviprrrg	1146		
QY	61	SKTLAAKPKPPTQMTYVDDDLVGMPPRPARRSLTPTCGSSDLVLTNRADVLPVRRG	120		
Db	1147	dsrgslisprpisyksssggpllcpvghavglfiraavctrgvakavdflpvenletmr	1206		
QY	121	DSRGSLSLSPREVSYLKSGSGPLLCPRGHAGIRPAVCIIRGVAKADVPVSEMETMR	180		
Db	1207	spvfdnsspparpgsfvahlhaptsgsktkryaayaakqyvvlylinsvaatlqfga	1266		
QY	181	SPVPTDSSPPAPVQSPFVAHLHAPTGSKSTKYPAAYAAOGKYVLVYNPVAATLFGA	240		
Db	1267	ymskahygdplirgvtrilttgspltystygkfladagcsgayadlilicdehstdatsi	1326		
QY	241	YMSKAHGIDPNIRIGSVRITTGAPVYTSYTGKFLADGCSGAGADIIICDECHSTDSTTI	300		
Db	1327	sgigtvldgaetagarlvvlatappgsvtrshpnieevalsttgelpfygkajlpvrik	1386		
QY	301	LGIGTVLDQAEFAGARLVVLATAPPGSVTPHPNIEEVALSNNGELPFYKALPIEAIR	360		
Db	1387	ggrhlifchskkkcdelaaklvalglnavayrrgldvsvldpsgvgvvsdaalmtgftg	1446		
QY	361	GGRHLIFCHSKKKCDDELALabel= Cys, Arg			
FT	Misc_difference 246				
FT	/label= Leu, Phe				
FT	Misc_difference 263				
FT	/label= Asp, Asn				
FT	Misc_difference 291				
FT	/label= Phe, Ser				
FT	Misc_difference 311				
FT	/label= Gly, Asp				
FT	Misc_difference 398				
FT	/label= Ser, Arg, Gly				
FT	Misc_difference 400				
FT	/label= Thr, Ala				
FT	Misc_difference 405				
FT	/label= Glu, Pro, Leu				
FT	Misc_difference 410				
FT	/label= Lys, Arg				
FT	Misc_difference 418				
FT	/label= Gly, Asp				
FT	Misc_difference 430				
FT	/label= Asn, Asp				
FT	Misc_difference 438				
FT	/label= Phe, Leu				
FT	Misc_difference 478				
FT	/label= Arg, Lys				
FT	Misc_difference 759				
FT	/label= Leu, Val				
FT	Misc_difference 1017				
FT	/label= Ser, Asn				
FT	Misc_difference 1036				
FT	/label= Thr, Ala				
FT	Misc_difference 1056				
FT	/label= Glu, Asp				
FT	Misc_difference 1201				

FT /label= Met, Thr
FT Misc.difference 1205
FT /label= Met, Ile
FT Misc.difference 1255
FT /label= Asn, Tyr
FT Misc.difference 1263
FT /label= Gly, Asp
FT Misc.difference 1455
FT /label= Asn, Asp
FT Misc.difference 1828
FT /label= Ala, Thr
FT Misc.difference 1895
FT /label= Gly, Arg
FT Misc.difference 1896
FT /label= Gly, Ile
FT Misc.difference 2143
FT /label= Glu, Val
FT Misc.difference 2144
FT /label= Asp, Glu
FT Misc.difference 2462
FT /label= Cys, Arg
FT Misc.difference 2486
FT /label= Val, Met
FT Misc.difference 2488
FT /label= Lys, Gln
FT Misc.difference 2844
FT /label= Leu, Met
FT Misc.difference 2862
FT /label= Leu, Gln
FT Misc.difference 2917
FT /label= Arg, Leu
FT Misc.difference 2968
FT /label= Ser, Gly
FT Misc.difference 2989
FT /label= Cys, Arg
FT Misc.difference 2990
FT /label= Tyr, Cys
PN J06105690-A.
PD 19-APR-1994.
PF 10-MAR-1992; 051885.
PR 10-MAR-1992; JP-051885.
PA (KAEV/) KAEVNO K.
DR WPI; 94-163130/20.
DR N-PSDB; 063499.
PT Blood-transmissible non-A non-B hepatitis virus DNA - used for
PM detection of hepatitis virus
PS Claim 1; Page 8-20; 22pp; Japanese.
CC This sequence is encoded by the genome of a blood transmissible non-A,
CC non-B hepatitis (NANBH) virus. The cDNA sequence was isolated using the
CC primers given in 063500-35. The amplified fragments are used in the
CC detection of hepatitis virus. The target DNA was isolated from serum
CC of chronically infected NANBH patients who were C100 antibody-positive
CC and HCV RNA (NS5 region) positive. Reverse transcription-PCR and PCR
CC were performed on cDNA and the total hum

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CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; L06322; G192943; -
 DR EMBL; L07271; -; NOT_ANNOTATED_CDS.
 DR EMBL; L11064; G348247; -
 DR EMBL; S65335; G432326; -
 DR EMBL; S66181; G435782; -
 DR PIR; S37807; S37807.
 DR PIR; B48227; B48227.
 DR GCRDB; GCR_0229; -
 DR GCRDB; GCR_0493; -
 DR GCRDB; GCR_0634; -
 DR GCRDB; GCR_0642; -
 DR PROSITE; PS00237; G-PROTEIN_RECEPTOR.
 DR G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
 KW PROSPORylation; LIPOPROTEIN; PALMITATE.
 FT DOMAIN 1 45
 FT TRANSMEM 46 75
 FT TRANSMEM 76 84
 FT TRANSMEM 85 102
 FT TRANSMEM 103 124
 FT TRANSMEM 125 144
 FT TRANSMEM 145 174
 FT TRANSMEM 175 190
 FT TRANSMEM 191 215
 FT TRANSMEM 216 238
 FT TRANSMEM 239 261
 FT TRANSMEM 262 284
 FT TRANSMEM 285 293
 FT TRANSMEM 294 310
 FT TRANSMEM 311 372
 FT DOMAIN 18 18
 FT CARBOHYD 33 33
 FT CARBOHYD 121 198
 FT DISULFID 333 333
 FT LIPID 372 AA; 40561 MW; 5140222P5 CRC32;
 SQ SEQUENCE

Query Match 100.0%; Score 2743; DB 7; Length 372;
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MEVPSARAEIGSSPLVNLSDAFPSAPSGANASGSPGARSASIALAIALTALYSVC 60
 QY 1 MEVPSARAEIGSSPLVNLSDAFPSAPSGANASGSPGARSASIALAIALTALYSVC 60
 Db 61 AVGLIGNVLMFGIVRYTKLKTATNIIYFNALDALATSTLPQSAKYMETWPFGEEL 120
 QY 61 AVGLIGNVLMFGIVRYTKLKTATNIIYFNALDALATSTLPQSAKYMETWPFGEEL 120
 Db 121 CKAVLSIDYNNMFSIFLTMMSVDRIYAVCHPVKALDFRPAKAKLINICIWLASGVG 180
 QY 121 CKAVLSIDYNNMFSIFLTMMSVDRIYAVCHPVKALDFRPAKAKLINICIWLASGVG 180
 Db 181 VPIWMVAVTQPRDGAIVCMLOFPSPSWMDIVTKICVLFVAVPILITTVCYGIMLRL 240
 QY 181 VPIWMVAVTQPRDGAIVCMLOFPSPSWMDIVTKICVLFVAVPILITTVCYGIMLRL 240
 Db 241 TSVYLLSAGSKKDSIRITITMVLVVGAFVVCWAPLHIFIVTLVGINRRDPLVVAL 300
 QY 241 TSVYLLSAGSKKDSIRITITMVLVVGAFVVCWAPLHIFIVTLVGINRRDPLVVAL 300
 Db 301 HLCIALGYANSSINPVYAFIDENKRCFRCPCGRQSGRLRRRGQATTBREVTAC 360
 QY 301 HLCIALGYANSSINPVYAFIDENKRCFRCPCGRQSGRLRRRGQATTBREVTAC 360
 Db 361 TPSDGPGGGAAA 372
 QY 361 TPSDGPGGGAAA 372

RESULT 2 STANDARD; PRT; 372 AA.
 ID OPERA RAT
 AC P33533;

DT 01-FEB-1994 (REL. 28, CREATED)
 DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE DELTA-TYPE OPIOID RECEPTOR (DOR-1) (OPIOID RECEPTOR A).
 GN ROR-A.
 OS RATTUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE; 93351652.
 RA FUKUDA K., KATO S., MORI K., NISHI M., TAKESHIMA H.;
 RL FEBS LETT. 327:311-314(1993).
 RP [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
 RX MEDLINE; 94322412.
 RA ABOOD M.E., NOEL M.A., FARNSWORTH J.S., TAO Q.;
 RL J. NEUROSCI. RES. 37:714-719(1994).
 RL -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
 ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. HIGHLY
 STEREOSELECTIVE. RECEPTOR FOR ENKEPHALINS.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; U00475; G391865; -
 DR EMBL; U00475; G514211; -
 DR PIR; S34592; S34592.
 DR GCRDB; GCR_0638; -
 DR GCRDB; GCR_0805; -
 DR PROSITE; PS00237; G-PROTEIN_RECEPTOR.
 DR G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
 KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
 FT DOMAIN 1 45
 FT TRANSMEM 46 75
 FT TRANSMEM 76 84
 FT TRANSMEM 85 102
 FT TRANSMEM 103 124
 FT TRANSMEM 125 144
 FT TRANSMEM 145 174
 FT TRANSMEM 175 190
 FT TRANSMEM 191 215
 FT TRANSMEM 216 238
 FT TRANSMEM 239 261
 FT TRANSMEM 262 284
 FT TRANSMEM 285 293
 FT TRANSMEM 294 310
 FT TRANSMEM 311 372
 FT CARBOHYD 18 18
 FT CARBOHYD 33 33
 FT DISULFID 121 198
 FT LIPID 333 333
 FT SEQUENCE 372 AA; 40449 MW; 59F5EB50 CRC32;
 SQ SEQUENCE

Query Match 96.9%; Score 2657; DB 7; Length 372;
 Best Local Similarity 97.0%; Pred. No. 0.00e+00;
 Matches 361; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Db 1 MEVPSARAEIGSSPLVNLSDAFPSAPSGANASGSPGARSASIALAIALTALYSVC 60
 QY 1 MEVPSARAEIGSSPLVNLSDAFPSAPSGANASGSPGARSASIALAIALTALYSVC 60
 Db 61 AVGLIGNVLMFGIVRYTKLKTATNIIYFNALDALATSTLPQSAKYMETWPFGEEL 120
 QY 61 AVGLIGNVLMFGIVRYTKLKTATNIIYFNALDALATSTLPQSAKYMETWPFGEEL 120
 Db 121 CKAVLSIDYNNMFSIFLTMMSVDRIYAVCHPVKALDFRPAKAKLINICIWLASGVG 180
 QY 121 CKAVLSIDYNNMFSIFLTMMSVDRIYAVCHPVKALDFRPAKAKLINICIWLASGVG 180
 Db 181 VPIWMVAVTQPRDGAIVCMLOFPSPSWMDIVTKICVLFVAVPILITTVCYGIMLRL 240
 QY 181 VPIWMVAVTQPRDGAIVCMLOFPSPSWMDIVTKICVLFVAVPILITTVCYGIMLRL 240

SEQUENCE FROM N.A.
MEDLINE; 95107267.
SIMONIN F., BEFORT K., GAVERLUX-ROUF C., MATTHES H., NAPPEY V.,
LANNES B., MICHELLETTI G., KIEFFER B.,
MOL. PHARMACOL. 46:1015-1021(1994).
-1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. HIGHLY
SPECIFIC SELECTIVE RECEPTOR FOR ENKEPHALINS.
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
EMBL; U07882; G497314; -
EMBL; U10504; E162517; -
MIM; 165195; -
PROSITE; PS00237; G-PROTEIN RECEPTOR.
G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
DOMAIN 1 45
TRANSSEM 46 75
DOMAIN 76 84
TRANSSEM 85 102
DOMAIN 103 124
TRANSSEM 125 144
DOMAIN 145 174
TRANSSEM 175 190
DOMAIN 191 215
TRANSSEM 216 238
DOMAIN 239 261
TRANSSEM 262 284
DOMAIN 285 293
TRANSSEM 294 310
DOMAIN 311 372
CARBOHYD 18 18
CARBOHYD 33 33
DISULFID 121 121
LIPID 121 198
CONFLICT 27 27
CONFLICT 333 333
CONFLICT 40 41
CONFLICT 348 348
CONFLICT 370 370
SEQUENCE 372 AA; 40450 MW; CFP92885 CRC32:
EXTRACELLULAR (POTENTIAL).
1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
BY SIMILARITY.
PALMITATE (POTENTIAL).
F -> C (IN REF. 2).
FG -> AR (IN REF. 2).
F -> A (IN REF. 2).
R -> A (IN REF. 2).
CFP92885 CRC32:

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RESULT      4
ID          AC          P35372;          STANDARD;          PRT;          400 AA.
OC          OPRL_HUMAN
RN          DT          01-JUN-1994 (REL, 29, CREATED)
DT          01-JUN-1994 (REL, 29, LAST SEQUENCE UPDATE)
DT          01-NOV-1995 (REL, 32, LAST ANNOTATION UPDATE)
DE          M $\mu$ -TYPE OPIOID RECEPTOR (MOR-1).
GN          OPRM1 OR MOR1.
OS          HOMO SAPIENS (HUMAN).
OC          EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC          EUTHERIA; PRIMATES.
RN          [1]
RP          SEQUENCE FROM N.A.
RC          TISSUE-BRAIN:
RX          MEDLINE: 94139928.
RA          WANG J.-B., JOHNSON P.S., PERSICO A.M., HAWKINS A.L., GRIFFIN C.A.,
RA          UHL G.R.;
RN          FEBS LETT. 338:217-222(1994).
[2]
RP          SEQUENCE FROM N.A.
RC          TISSUE-BRAIN:
RA          MESTEK A. JR., HURLEY J.H., BYE L.S., CAMPBELL A., TIAN M.,
RA          CHEN Y., YU L.;
RN          SUBMITTED (XXK-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
CC          -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC          ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
CC          FOR BETA $\mu$ -ENDORPHIN.
CC          -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
CC          -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR          EMBL, L25119; G452073;
DR          EMBL, L29301; G459852;
DR          GCRDB, GCR_0885;
DR          GCRDB, GCR_0985;
DR          MIM, 600018;
DR          PROSITE, PS00237; G-PROTEIN RECEPTOR.
DR          G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
ET          PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
ET          DOMAIN
ET          TRANSMEM 1 66
ET          67 96
ET          1 (POTENTIAL).

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ID	OPRM_MOUSE	STANDARD:	PRT:	398 AA.
AC	P42866;			
DT	01-NOV-1995 (REL. 32, CREATED)			
DT	01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)			
DT	01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)			
GN	MOR.			
GN	MUS MUSCULUS (MOUSE).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; RODENTIA.			
RC	(1)			
RC	SEQUENCE FROM N.A.			
RC	STRAIN-C57BL/6; TISSUE-LIVER;			
RC	MEDLINE: 94377496.			
RA	MIN B.H., AUGUSTIN L.B., FELSHEIM R.F., FUCHS J.A., LOH H.H.;			
RA	PROC. NATL. ACAD. SCI. U.S.A. 91:9081-9085(1994).			
RP	(12)			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-BRAIN:			
RC	MEDLINE: 95377399.			
RA	ROSSI G.C., PAN Y.X., BROWN G.P., PASTERNAK G.W.;			
RL	FEBS LETT. 369:192-196(1995).			
CC	-1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM			
CC	ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR			
CC	FOR BETA-ENDORPHIN.			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
DR	EMBL; U10561; G565069; -.			
DR	EMBL; U10558; G565069; JOINED.			
DR	EMBL; U10559; G565069; JOINED.			
DR	EMBL; U10560; G565069; JOINED.			
DR	EMBL; U26915; G105523; -.			
DR	PROSITE: PS00237; G-PROTEIN RECEPTOR.			
KW	G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;			
KW	PHOSPHORYLATION; LIPOPROTEIN; PALMITATE			
FT	DOMAIN 1 64			
FT	TRANSMEM 65 94			
FT	DOMAIN 95 103			
FT	TRANSMEM 104 103			
FT	DOMAIN 104 121			
FT	TRANSMEM 122 143			
FT	DOMAIN 144 163			
FT	TRANSMEM 164 193			
FT	DOMAIN 194 209			
FT	TRANSMEM 210 234			
FT	DOMAIN 235 257			
FT	TRANSMEM 258 280			
FT	DOMAIN 281 303			
FT	TRANSMEM 304 311			
FT	DOMAIN 312 328			
FT	TRANSMEM 329 398			
FT	DOMAIN 398			
FT	CYTOPLASMIC (POTENTIAL).			
FT	EXTRACELLULAR (POTENTIAL).			
FT	1 (POTENTIAL).			
FT	CYTOPLASMIC (POTENTIAL).			
FT	2 (POTENTIAL).			
FT	EXTRACELLULAR (POTENTIAL).			
FT	3 (POTENTIAL).			
FT	CYTOPLASMIC (POTENTIAL).			
FT	4 (POTENTIAL).			
FT	EXTRACELLULAR (POTENTIAL).			
FT	5 (POTENTIAL).			
FT	CYTOPLASMIC (POTENTIAL).			
FT	6 (POTENTIAL).			
FT	EXTRACELLULAR (POTENTIAL).			
FT	7 (POTENTIAL).			
FT	CYTOPLASMIC (POTENTIAL).			

ID	OPRK	RAT	STANDARD:	PRT:	380	AA.
AC	P34975,					
DT	01-FEB-1994	(REL. 28,	CREATED)			
DT	01-FEB-1994	(REL. 28,	LAST SEQUENCE UPDATE)			
DT	01-FEB-1996	(REL. 33,	LAST ANNOTATION UPDATE)			
DE	KAPPA-TYPE OPIOID RECEPTOR	(KOR-1),				
GN	ROR-D.					
OS	RATUUS NORVEGICUS (RAI).					
OC	EUKARIOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
OC	EUTHERIA; ROSENTIA.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE-BRAIN:					
RA	MEDLINE; 94059008.					
RA	CHEN Y., MESTER A., LIU J., YU L.,					
RL	BIOCHEM. J. 295:625-628 (1993).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE; 93374033.					
RA	MINAMI M., TOYA T., KATAO Y., MAEKAWA K., NAKAMURA S., ONOGI T.,					
RA	KANEKO S., SATOH M.,					
RL	FEBS LETT. 329:291-295 (1993).					
RN	[3]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;					
RX	MEDLINE; 94059009					
RA	LI S., ZHU J., CHEN C., CHEN Y.-W., DERIEDL J.K., ASHBY B.,					
RA	LID-CHEN L.-Y.,					
RL	BIOCHEM. J. 295:629-633 (1993).					
RN	[4]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;					
RX	MEDLINE; 94052210.					
RA	MENG F., XIE G.-X., THOMPSON R.C., MANSOUR A., GOLDSTEIN A.,					
RA	WATSON S.-J., AKIL H.,					

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RL PROC. NATL. ACAD. SCI. U.S.A. 90:9954-9958(1993).
RN
RN [5]
RC SEQUENCE FROM N.A.
RC STRAIN-WISTAR: TISSUE-BRAIN;
RX MEDLINE; 93380575.
RA NISHI M., TAKESHIWA H., FUKUDA K., KATO S., MORI K.;
RA FEBS LETT. 330:77-80(1993).
RN
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RX MEDLINE; 95204422.
RA YAKOVLEV A.G., KRUEGER K.E., FADEN A.I.;
RA J. BIOL. CHEM. 270:6421-6424(1995).
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
CC FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF
CC AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; L22001: G409237; -
DR EMBL; D16829: G404116; -
DR EMBL; L22536: G425189; -
DR EMBL; U00442: G403487; -
DR EMBL; D16534: G415310; -
DR EMBL; U17995: G727260; -
DR EMBL; U17993: G727260; JOINED.
DR EMBL; U17994: G727260; JOINED.
DR PIR; S36143; S36143.
DR PIR; S38825; S38825.
DR GCRDB; GCR 0636; -
DR GCRDB; GCR 0724; -
DR GCRDB; GCR 0790; -
DR GCRDB; GCR 0804; -
DR PROSITE; PS00237; G-PROTEIN RECEPTOR.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 58
FT TRANSSEM 59 85
FT TRANSSEM 96 95
FT TRANSSEM 118 117
FT TRANSSEM 133 132
FT TRANSSEM 155 154
FT TRANSSEM 174 196
FT TRANSSEM 197 222
FT TRANSSEM 223 247
FT TRANSSEM 248 275
FT TRANSSEM 276 299
FT TRANSSEM 300 311
FT TRANSSEM 312 333
FT TRANSSEM 334 380
FT DISULFD 131 210
FT LIPID 345 345
FT CARBOHYD 25 25
FT CARBOHYD 39 39
FT CONFLICT 42 42
FT CONFLICT 45 45
FT CONFLICT 345 345
FT CONFLICT 42688 MW; E858A46 CRC32;
SQ SEQUENCE 380 AA; 42688 MW;

Query Match 58.5%; Score 1604; DB 7; Length 380;
Best Local Similarity 67.0%; Pred. No. 0.00e+00;
Matches 207; Conservative 51; Mismatches 45; Indels 6; Gaps 5;

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QY 167 LTNICWIASGVGPIWMAYTQPRDGA-VY-CMLQFSP--SWWPDVTKICVLEPAF 222
DB 236 vlpvllivcytlmllrksvlllgstrekdnrltrfklyvvavvflcctphlfi 295
QY 223 vvpillitwcygmllrlrsvrlsgskrdslnrltmvllvvgafvcpvphlfi 282
DB 296 valsgstgsta-vlssxyfcalqytinaslrvlyafidenfkicrficfpikmmer 354
QY 283 vvlvndlnrddvlyaaahcltalgtanslnpvlafidenfkrcfrcpccgrop 342
DB 355 gslrrpqa 351
QY 343 gslrrpqa 351

RESULT 8
ID OPRK_HUMAN STANDARD; PRT; 380 AA.
AC P41145;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE KAPPA-TYPE OPIOID RECEPTOR (KOR-1).
GN OPRK1 OR OPRK.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PLACENTA;
RX MEDLINE; 9438360.
RA MANSON E., BARE L.A., YANG D.;
RA BIOCHEM. BIOPHYS. RES. COMMUN. 202:1431-1437(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-PLACENTA;
RX MEDLINE; 95350200.
RA SIMONIN F., GAVRIANUS-RUFF C., BEFORT K., LANNES B., MICHELETTI G.,
RA MATTEI M.-G., CHARON G., BLOCH B., KIEFFER B.;
RA PROC. NATL. ACAD. SCI. U.S.A. 92:7006-7010(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE; 95174504.
RA ZHU J., CHEN C., XUE J.C., KUNAPULI S., DERIEL J.K., LIU-CHEN L.-Y.;
RA LIFE SCI. 56:201-207(1995).
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
CC FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF
CC AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; U1053: G532060; -
DR EMBL; U17298: G536070; -
DR EMBL; L37362: G722618; -
DR PIR; JC2338; JC2338.
DR MIM; 165196; -.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 58
FT TRANSSEM 59 85
FT TRANSSEM 86 95
FT TRANSSEM 118 117
FT TRANSSEM 133 132
FT TRANSSEM 155 154
FT TRANSSEM 174 196
FT TRANSSEM 197 222
FT TRANSSEM 223 247
FT TRANSSEM 248 275
FT TRANSSEM 276 299
FT TRANSSEM 300 311
FT TRANSSEM 312 333

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ID	OPRK	CAVPO	STANDARD:	PRT:	380 AA.
DT	01-FEB-1995	(REL. 31, LAST SEQUENCE UPDATE)			
DT	01-FEB-1995	(REL. 31, LAST SEQUENCE UPDATE)			
DT	01-NOV-1995	(REL. 32, LAST ANNOTATION UPDATE)			
DT	KAPPA-TYPE OPIOID RECEPTOR (KOR-1)				
CC	-! SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
DR	EMBL	L11065; G348249; -			
DR	EMBL	D31665; G808876; -			
DR	EMBL	D31663; G808876; JOINED.			
DR	EMBL	D31664; G808876; JOINED.			
DR	EMBL	S77872; G998532; JOINED.			
DR	EMBL	S77868; G998532; JOINED.			
DR	EMBL	S77869; G998532; JOINED.			
DR	PIR	A48227; A48227.			
DR	GCRDB	GCR_0635; -			
DR	PROSITE	PS00237; G-PROTEIN_RECEPTOR.			
KW	G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;				
KW	PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.				
FT	DOMAIN	1	58		EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	59	85		1 (POTENTIAL).
FT	DOMAIN	86	95		CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	96	117		2 (POTENTIAL).
FT	DOMAIN	118	132		EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	133	154		3 (POTENTIAL).
FT	DOMAIN	153	173		CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	174	196		4 (POTENTIAL).
FT	DOMAIN	197	222		EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	223	247		5 (POTENTIAL).
FT	DOMAIN	248	275		CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	276	299		6 (POTENTIAL).
FT	DOMAIN	300	311		EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	312	333		7 (POTENTIAL).
FT	DOMAIN	334	380		CYTOPLASMIC (POTENTIAL).
FT	DISULFID	131	210		BY SIMILARITY.
FT	LIPID	345	345		PALMITATE (POTENTIAL).
FT	CARBOHYD	25	25		POTENTIAL.
FT	CARBOHYD	39	39		POTENTIAL.
FT	CONFLICT	211	211		S -> L (IN REF. 2 AND 3).
FT	CONFLICT	231	231		F -> V (IN REF. 2 AND 3).
FT	SEQUENCE	380 AA;	42652 MM;	C6S3212 CRC32;	
Query Match					
Best Local Similarity 66.7%; Pred. No. 0.00e+00;					
Matches 206; Conservative 51; Mismatches 46; Indels 6; Gaps 5					
Db	57	alpvlttavyvsvfvvgvlgvnslnvfvflllyrtkmtatnlyiflajaladalvtltmpfgs	116		
QY	47	ALAAILTALYSVCVAVGGLGVLVWFGVGRVTKLKLAININIIEMLAADALATSTLDFQS	106		
Db	117	avylmmswpfgvdlcklvisldyyumfscftlltmmsvdxrylavychvkaaldfttpjak	176		
QY	107	AKYLEIETWPFGLCKAVLSIDYINMTFSITTLIMASVDRIIAVCHVKALDFETPAKAK	166		
Db	177	lindliwllassvylsaivlggtkyredvdlceslqfddpdeysw-vdlfmkicvfyfaf	235		
QY	167	LINICIIWLVAGVGPVIMVMAVTPORPGA-VV-CMLQFPPS-SWMYDYTKICVFEFAF	222		
Db	236	vlpvllivvcytlmlalrtksvrlisgsrrednmlrtklvlyvvavaficwtprhlfel	295		
QY	223	VPLIILIVVCGLMLIRKSRVRLISGSKEDRSIRRTTRVLYVVGAFVCMAPRIHIFVI	282		
Db	296	vealgsstshsta-alsysyfcialygnslmplyafldentKkrofdcfcpikmmer	354		
QY	283	WVILVDIRPDPVLYVALHLCIALGYNSSLNVLYAFIDENKRCRFRQCRTPCGROEP	342		
Db	365	qsthrvnt	363		
QY	343	GLSLRRPROA	351		
RESULT	10				
ID	OPRK	CAVPO	STANDARD:	PRT:	380 AA.
AC	P41144;				

ID	OPR	HUMAN	STANDARD	PRT	370 AA
AC	P41146				
CC		ENKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC		EUTHERIA; RODENTIA.			
RN		[1]			
RP		SEQUENCE FROM N.A.			
RC		STRAIN-HARTLEY; TISSUE-BRAIN;			
RX		MEDLINE; 94224925.			
RA		XIN G. X., MENG F., MANSOUR A., THOMPSON R.C., HOVERSTEN M.T.,			
RA		GOLDSTEIN A., WATSON S.T., AKIL H.;			
RL		PROC. NATL. ACAD. SCI. U.S.A. 91:3779-3783(1994).			
CC		-1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM			
CC		ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR			
CC		FOR DYSOPHENS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF			
CC		ATONOMIC AND NEUROENDOCRINE FUNCTIONS.			
CC		-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC		-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
DR		EMBL; U04092; G476107; -.			
DR		GCR 0991; -.			
DR		PROSITE; PS00237; G-PROTEIN RECEPTOR.			
KW		G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;			
KW		PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.			
FT		DOMAIN	1	58	EXTRACELLULAR (POTENTIAL).
FT		TRANSMEM	59	85	1 (POTENTIAL).
FT		DOMAIN	86	95	CYTOPLASMIC (POTENTIAL).
FT		TRANSMEM	96	117	2 (POTENTIAL).
FT		DOMAIN	118	132	EXTRACELLULAR (POTENTIAL).
FT		TRANSMEM	133	154	3 (POTENTIAL).
FT		DOMAIN	155	173	CYTOPLASMIC (POTENTIAL).
FT		TRANSMEM	174	196	4 (POTENTIAL).
FT		DOMAIN	197	222	EXTRACELLULAR (POTENTIAL).
FT		TRANSMEM	223	247	5 (POTENTIAL).
FT		DOMAIN	248	275	CYTOPLASMIC (POTENTIAL).
FT		TRANSMEM	276	299	6 (POTENTIAL).
FT		DOMAIN	300	311	EXTRACELLULAR (POTENTIAL).
FT		TRANSMEM	312	333	7 (POTENTIAL).
FT		DOMAIN	334	380	CYTOPLASMIC (POTENTIAL).
FT		DISULFID	131	210	BY SIMILARITY.
FT		LIPID	345	345	PALMITATE (POTENTIAL).
FT		CARBOHYD	25	25	POTENTIAL.
FT		CARBOHYD	39	39	POTENTIAL.
SO		SEQUENCE	380 AA;	42736 MW;	F9F34C4C CRC32;
Query Match			58.0%;	Score 1592;	DB 7; Length 380;
Best Local Similarity			64.9%;	Pred. No. 0.0e+00;	
Matches		200;	Conservative	55;	Mismatches 49; Indels 4; Gaps 4;
Db	57	alpvlltavyvsvfvvgvlgvsglvmfvilrtykmtkatchiyfnlalnadalvtttmfpgs	116		
Qy	47	ALMAIATATYSAVCAVGLGAVLGNVLVMGVIKRYTKLKNATNVIYFNALADALATSTLPRQS	106		
Db	117	tvylmmswpgfdvclctkvtlsidgymfetsiflltmssvrvyiaavchprkaldfrtprkak	176		
Qy	107	AKYIMEMWPGELICAKAVLSIDYNNFTSLFTLTMASVDRIYAVCHPRKALDFRRPAKAK	166		
Db	177	llhlccllssvgsiaalllgvltkfredvdllecsiqfdddysswdlfmklcvfvafv	236		
Qy	167	LINICIVLWLSGCVPLMMVAVYQPPDGA-VV-CMLQPSPSGW-XWDYVTKICVLPFAFV	223		
Db	237	ipvlllvcytlmlrlrksvrllsgsfrekdnrlrrltlrvlyvavafllcwprlhhllly	296		
Qy	224	VPILITIVCYGIMLRLRVSRLLSGSEKERSLRRTTRWLVVVGAVVCMAPDIIIEYIV	283		
Db	297	ealstshstla-alsstyfcclaygtmsslnpllyflidenfkrcfrdcfcfpikmmernq	355		
Qy	284	WLVLDINRDLVVAALHLCIALGYANSSLNPFVLAIFDENFKRCRQLCRPPCGSGDENG	343		
Db	356	stsvrynt 363			
Qy	344	STRPRQA 351			
RESULT	11				
ID	OPR	HUMAN	STANDARD	PRT	370 AA
AC	P41146				

[illegible]

DR	EMBL	U01913	G487965	-	
DR	EMBL	L28144	G496220	-	
DR	EMBL	U07871	G606803	-	
DR	EMBL	L39116	G557200	-	
DR	EMBL	L29419	G510719	-	
DR	PIR	S46238	S46238	-	
DR	PIR	S43655	S43655	-	
DR	GCRDB	GCR_0834	-		
DR	GCRDB	GCR_0898	-		
DR	GCRDB	GCR_0912	-		
DR	PROSITE	PS00237	G_PROTEIN_RECEPTOR		
KW	G-PROTEIN COUPLED RECEPTOR	TRANSMEMBRANE	GLYCOPROTEIN		
KW	PHOSPHORYLATION	LIPOPROTEIN	PALMITATE		
FT	DOMAIN	1	47		
FT	TRANSMEM	48	74		
FT	DOMAIN	75	84		
FT	TRANSMEM	85	106		
FT	DOMAIN	107	121		
FT	TRANSMEM	122	143		
FT	DOMAIN	144	162		
FT	TRANSMEM	163	185		
FT	DOMAIN	186	208		
FT	TRANSMEM	209	233		
FT	DOMAIN	234	261		
FT	TRANSMEM	262	285		
FT	DOMAIN	286	297		
FT	TRANSMEM	298	319		
FT	DOMAIN	320	366		
FT	DISULFID	120	197		

Seq primer: -28M13 rev2 from Amersham

High quality sequence stop: 262.

Location/Qualifiers

1..358

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/organism="Homo sapiens"  

/note="Organ: heart; Vector: pT733 (Pharmacia) with a  

modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st  

strand cDNA was primed with a Not I - oligo(dT) primer  

TGTTTCACATCTGAAAGTAGAGCGGCCGCACCATTCTTTTTTTTTTTT  

double-stranded cDNA was size selected, ligated to Eco  

adapters (pharmacial), digested with Not I and cloned in  

the Not I and Eco RI sites of a modified pT73 vector  

(Pharmacia). Library went through one round of  

normalization to a Cot = 5. Library constructed by  

M.Patima Bonaldo. This library was constructed from the  

same fetus as the fetal lung library, Soares fetal lung  

NBHL19W."  

Nhlw19W."  

/clonelib="Soares fetal heart NBHL19W"  

/sex="unknown"  

/dev_stage="19 weeks"  

/lab_host="DHIOB (ampicillin resistant)"  

<1..>338  

BASE COUNT      65 a       115 c        67 g         89 t          2 others  
ORIGIN
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Dt Query Match Best Local Similarity 98.2%; Pred No. 0.00e+00; Matches 330; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Dd 3 ggagccctttcatcattacactgctcttccttacctcgagtgaccttatcatatggaccanaaat 62 QY 384 GGCCCCCTTTCATCCTACTGGCTGTCTTCACTCCGAGGSCCTTATCATAGGCCACAATAA 443 Dd atgaatttagctcaagtgcgatatacaatttgtgaacctgscotgatctgtcaatcaticc 122 QY 444 ATGAATTACGTCACAGTGGCATACAGATGGAGCACCTCGCATGTGCATGCATCAATCC 503 Db actaacacaagaaggcctctgtaaaaggcctcttgtaaaccgctctccccatgygaactatgc 182 QY 504 ACTACATCAAGAAGCGCTCTGTGAAGCGCTCTTCGTGACACCGCTCTTCOCATGGACATATGC 563 Db ctcttgccaacattttaagaactgccaccctaactatggagcttgcggcgltgatggcct 242

QY 564 CTTTGGGACATCTTCAAGAACTGACACTACTGAGGCGCTTCCGCGGTGGATGGCCT 623

Db 243 attacaataacacctctctacactcccccactgaagagctgaagaaatg 302

QY 624 ATTACATCATACACCTCTCTACACTCCCTTACTGAGAGCTGAGCAAGTGAACATGG 683

Db 303 cgcctgaactcttctgactcgaagctcggaact 338

QY 684 CGCTGGCCATCTTTGTGATCTGCCAGCTGGGCAACT 719

RESULT 14
ID HSA040670 standard; RNA; EST; 338 BP.
AC AA040670;
NI 91516948
DT 31-AUG-1996 (rel. 49, Created)
DT 31-AUG-1996 (rel. 49, Last updated, Version 1)
DE z606a08.r1 Soares fetal heart NBH19W Homo sapiens cDNA clone
DE 376118 5' similar to PIR:S52504 S52504 homolog of rat synaptic
DE glycoprotein SC2 ; .
KW EST.
OS Homo sapiens (human)
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea.
RN 1-338
RP 1-338
RA Hillier L., Clark N., Dubuque T., Eliston K., Hawkins M.,
RA Holman M., Hulman M., Kucaba T., Le M., Lennon G., Merra M.,
RA Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,
RA Trevasakis E., Waterston R., Williamson A., Wohlmann P., Wilson R.,
RA "The WashU-Merck EST Project";
RT Unpublished
RU Contact: Wilson RK WashU-Merck EST Project Washington University
CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
CC est@wustl.wustl.edu This clone is available royalty-free through
CC LIND; contact the IMAGE Consortium (info@image.lind.gov) for
CC further information. Seq primer: -28M13 rev2 from Amerisham High
CC quality sequence stop: 262.
FH Key Location/Qualifiers
FT source
FT 1..338
FT /organism="Homo sapiens"
FT /note="Organ: heart; Vector: pT73D (Pharmacia) with a
FT modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st
FT strand cDNA was primed with a Not I - oligo(dT) primer [5'
FT TGTACCAATCTGAGTGGAGCGCGGCACTCTTTTCTTTTCTTTT 3']
FT TGTACCAATCTGAGTGGAGCGCGGCACTCTTTTCTTTTCTTTT 3']
FT double-stranded cDNA was size selected, ligated to Eco RI
FT adapters (Pharmacia), digested with Not I and cloned into
FT the Not I and Eco RI sites of a modified pT73 vector
FT (Pharmacia). Library went through one round of
FT normalization to a Cot = 5. Library constructed by M.Fatima
FT 2
FT Bonaldo. This library was constructed from the same fetus
FT as the fetal lung library, Soares fetal lung NBH19W."
FT /clone="376118"
FT /clone.lib="Soares fetal heart NBH19W"
FT /sex="unknown"
FT /dev_stage="19 weeks"
FT /lab_host="DH10B (ampicillin resistant)"
FT <1..>338
SQ Sequence 338 BP; 65 A; 115 C; 67 G; 89 T; 2 other;

Query Match 28.7%; Score 326; DB 229; Length 338;
Best Local Similarity 98.2%; Pred. No. 0.00e+00;
Matches 330; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 3 gggcccttcacatccgcctcttactcgaagtgccctcactatggccanaat 62
|||
QY 384 GGGCCCTTTTCATCTACGCTCTTCTACTTCGAGTGGCCCTTCATCTAAGCCACAAT 443
|||
Db 63 atgacttaacgtccagtcggacatacagtggtgactcgcctgcctcctatcatttc 122
|||

QY 444 ATGACTTACGTCACAGTGGGACATACAGNGTGTGCAACCTCGCTGCATCTGTCACTCATTC 503

Db 123 actacaataagcgctgctgtgaagagctcttcgtagaccgcttcctccatgacatgac 182

QY 504 ACTACATCAAGCGGCTGTGGAGAGAGCTTTCGTGACACGCTTCTCCATGCACTAATGC 563

Db 163 ctttgcgaacactcttaagaactgacactactactggtggttcgcgcgttgatgagcct 242

QY 564 CTTTGGGACATCTTCAAGAACTGACACTACTGAGGCGCTTCCGCGGTGGATGGCCT 623

Db 243 attacaataacacctctctacactcccccactgaagagctgaagaaatg 302

QY 624 ATTACATCATACACCTCTCTACACTCCCTTACTGAGAGCTGAGCAAGTGAACATGG 683

Db 303 cgcctgaactcttctgactcgaagctcggaact 338

QY 684 CGCTGGCCATCTTTGTGATCTGCCAGCTGGGCAACT 719

RESULT 15
LOCUS R48780 387 bp mRNA EST 18-MAY-1995
DEFINITION YJ69C08.s1 Homo sapiens cDNA clone 153998 3' similar to
SP:S5A2_HUMAN P31213 3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 2 ; .
ACCESSION R48780
NTD R48780
KEYWORDS EST.
SOURCE human clone=153998 library=Soares breast 2NDBst vector=pT73D
DESCRIPTION (Pharmacia) with a modified polylinker host=DH10B (ampicillin
resistant) primer=Promega -21M13 Rsite1-Not I Rsite2-Eco RI Adult
female. 1st strand cDNA was primed with a Not I - oligo(dT) primer
[5' TGTACCAATCTGAGTGGAGCGCGGCACTCTTTTCTTTTCTTTT 3']
[5' TGTACCAATCTGAGTGGAGCGCGGCACTCTTTTCTTTTCTTTT 3']
double-stranded cDNA was ligated to Eco RI adapters (Pharmacia),
digested with Not I and cloned into the Not I and Eco RI sites of a
modified pT73 vector (Pharmacia). Library went through one round
of normalization to a Cot = 230. Library constructed by Bento
Soares and M.Fatima Bonaldo.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
XX
AC xxxxxx
DT 01-JAN-1900
XX Sequence 36, Application US/07769996C.
DS Sequence 36, Application US/07769996C.
XX
CC Sequence 36, Application US/07769996C
CC GENERAL INFORMATION:
CC APPLICANT: OKAYAMA, Hiroto
CC APPLICANT: FUKE, Isao
CC APPLICANT: MORI, Chisato
CC APPLICANT: TAKAHIZAMA, Akahisa
CC APPLICANT: YOSHIDA, Iwao
CC TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
CC TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
CC NUMBER OF SEQUENCES: 50
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Armstrong, Westernman, Hattori, McIreland
CC ADDRESSEE: 6 Naughton
CC STREET: 1725 K St. N.W. Suite 1000
CC CITY: Washington
CC STATE: D.C.
CC COUNTRY: U.S.A.
CC ZIP: 20006
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/769,996C
CC FILING DATE: 02-OCT-1991

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CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: JP 2-167466
CC FILING DATE: 25-JUN-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: JP 2-230921
CC FILING DATE: 31-AUG-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: JP 2-305605
CC FILING DATE: 09-NOV-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/635,451
CC FILING DATE: 28-DEC-1990
CC ATTORNEY/AGENT INFORMATION:
CC NAME: McIeland, Le-Nhung
CC REGISTRATION NUMBER: 31,541
CC REFERENCE/DOCKET NUMBER: 900703B
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (202) 659-2930
CC TELEFAX: (202) 887-0357
CC INFO: 440142
CC INFORMATION FOR SEQ ID NO: 36:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 2621 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 2621 AA; 285007 MW; 36333929 CN;

Query Match
Best Local Similarity 100.0%; Score 4516; DB 11; Length 2621;
Matches 631; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 638 APTTASQGTGRLGTLITSLGRDKNQYGEVYVSTAFSGFLATCVNGVQWYVHGAG 697
QY 1 APTTASQGTGRLGTLITSLGRDKNQYGEVYVSTAFSGFLATCVNGVQWYVHGAG 60
Db 698 SKTLAAPKGPITOMTYNDQDLVGMFKPGARSLPCTGSSDLVYTHADYIPVRRRG 757
QY 61 SKTLAAPKGPITOMTYNDQDLVGMFKPGARSLPCTGSSDLVYTHADYIPVRRRG 120
Db 758 DSRGSLSPRVSYLKSSGGPLLPFGHANGIFRAVCTRGAKAVDPVPSMETMR 817
QY 121 DSRGSLSPRVSYLKSSGGPLLPFGHANGIFRAVCTRGAKAVDPVPSMETMR 180
Db 818 SPVETDSSPAVPSQVYAHAPTGSGSKTKVPAAYAAQGYKVLNPSVAATLGFGA 877
QY 181 SPVETDSSPAVPSQVYAHAPTGSGSKTKVPAAYAAQGYKVLNPSVAATLGFGA 240
Db 878 YMSKAHGIDPNIRGVRITTGAPVYTYSGKFLADGGSGGAYDIICDECHSDSTTI 937
QY 241 YMSKAHGIDPNIRGVRITTGAPVYTYSGKFLADGGSGGAYDIICDECHSDSTTI 300
Db 938 LGTGVLDQATAGARLVLAATAPPGSVTVPHNIEEVALSNTGEIPFYGAIPTEAIR 997
QY 301 LGTGVLDQATAGARLVLAATAPPGSVTVPHNIEEVALSNTGEIPFYGAIPTEAIR 360
Db 998 GGRLLIFCHSKKDELAARISGLGINAVYRGLDVSVPITGDVVVVATDALMTGYTG 1057
QY 361 GGRLLIFCHSKKDELAARISGLGINAVYRGLDVSVPITGDVVVVATDALMTGYTG 420
Db 1058 DEDSVINDCNTVLTQVDFSLDPTIETTPYPODAVSRSQRRGTGRRRGITVFVPG 1117
QY 421 DEDSVINDCNTVLTQVDFSLDPTIETTPYPODAVSRSQRRGTGRRRGITVFVPG 480
Db 1118 RPSGMPDSSVLCGECYDAGCAMYELTPAEISYRLRAYLNTFGLPYCQDHLFEWESVFTGLT 1177
QY 481 RPSGMPDSSVLCGECYDAGCAMYELTPAEISYRLRAYLNTFGLPYCQDHLFEWESVFTGLT 540
Db 1178 HIDAHFISQTKQAGNDPNYLVAYQATYCARAQAPPPSWDMWKILRLKPTLHGPPILY 1237
QY 541 HIDAHFISQTKQAGNDPNYLVAYQATYCARAQAPPPSWDMWKILRLKPTLHGPPILY 600
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Db 1238 RLGAQVQNEVLTTHPTIKYINAKMSADLEVVT 1268
QY 601 RLGAQVQNEVLTTHPTIKYINAKMSADLEVVT 631
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Search completed: Fri Jul 18 08:22:46 1997
Job time : 309 secs.

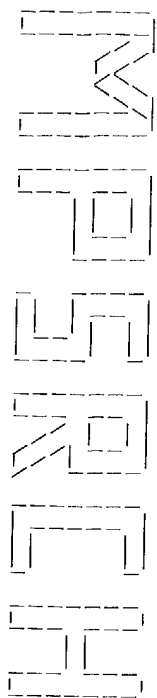
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FT TRANSMEM 166 188 POTENTIAL.
FT DOMAIN 189 212 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 213 237 POTENTIAL.
FT DOMAIN 238 245 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 246 270 POTENTIAL.
FT DOMAIN 271 283 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 284 300 POTENTIAL.
FT DOMAIN 301 311 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 312 329 POTENTIAL.
FT DOMAIN 330 488 PERIPLASMIC (POTENTIAL).
FT DISULFID 403 406 REDOX-ACTIVE (BY SIMILARITY).
FT CONFLICT 252 252 L -> V (IN REF. 1).
SQ SEQUENCE 488 AA; 52920 MW; FE6A2C9F CRC32;
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Query Match
Best Local Similarity 31.0%; Score 79; DB 3; Length 488;
Matches 13; Conservative 11; Mismatches 16; Indels 2; Gaps 2;

Db 92 walllgiglaftp-cvlpmyplisg-ivlgqkqristarall 131
QY 3 wlvvgvlnalaaayciltgsvivigriltsrpaivpdrll 44
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Search completed: Fri Jul 18 08:24:56 1997
Job time : 22 secs.

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(TM)

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MPsrch_bp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Aug 26 14:44:33 1997; Maspar time 10.17 Seconds
Tabular output not generated. 418.288 Million cell updates/sec

Title: >US-08-292-694A-4
Description: (1-372) from US08292694A.pep
Perfect Score: 2743
Sequence: 1 MELVPSARAEIQSSPIVMLS.....TREYVACTPSDGGGGAAA 372

Scoring table:
PAM 150
Gap 11

Searched: 96640 seqs, 11439865 residues

Post-Processing: Minimum Match 08
Listing first 45 summaries

Database:

a-geneseq27
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20

Statistics: Mean 34.833; Variance 155.441; scale 0.224

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description	Pred. No.
1	2743	100.0	372	13	Mouse delta opiod re	3.05e-247
2	2743	100.0	372	9	Sequence of murine de	3.05e-247
3	2650	96.6	372	14	Rat delta opiate rece	2.72e-238
4	2519	91.8	371	10	Murine delta opiate re	1.08e-150
5	1729	63.0	400	14	Human mu opiate recep	6.41e-125
6	1725	62.9	400	13	Human mu opiate recep	1.55e-149
7	1723	62.8	400	13	Rat mu opiate recep	2.40e-149
8	1721	62.7	356	11	Murine mu-subtype opi	3.72e-149
9	1721	62.7	356	14	Murine mu opiate recep	5.63e-138
10	1604	58.5	380	14	Mammalian kappa opioi	5.63e-138
11	1604	58.5	380	14	Rat kappa opiate rece	5.63e-138
12	1597	58.2	380	17	Human kappa opiod re	2.62e-137
13	1463	53.3	367	13	Mouse kappa opiod re	1.55e-124
14	1460	53.2	367	13	Human kappa opiod re	3.07e-124
15	1455	53.0	295	12	Mouse opiod receptor.	9.20e-124
16	1454	53.0	367	14	Human kappa opiod re	1.15e-123
17	1454	53.0	367	13	Rat opiorph receptor	2.68e-94
18	957	34.9	391	7	Human somatostatin re	1.57e-76
19	957	34.9	391	7	Murine somatostatin r	1.57e-76
20	957	34.9	391	7	Murine somatostatin r	1.57e-76

21	879	32.0	369	7	R39262	Murine somatostatin r	3.44e-69
22	873	31.8	333	13	R72985	Epsilon opiod recept	1.26e-68
23	871	31.8	369	19	R72859	Human somatostatin re	1.94e-68
24	871	31.8	369	7	R39261	Human somatostatin re	1.94e-68
25	869	31.7	369	5	R27504	Pituitary somatostati	3.00e-68
26	835	30.4	418	7	R39263	Human somatostatin re	4.66e-65
27	822	30.0	322	16	R48754	Rat RGH G-protein cou	7.71e-64
28	822	30.0	322	16	R48754	Rat RGH G-protein cou	7.71e-64
29	821	29.9	328	13	R2964	Epsilon opiod recept	9.57e-64
30	757	27.6	428	7	R39264	Murine somatostatin r	9.35e-58
31	605	22.1	349	14	R79443	Human galanin recepto	1.28e-43
32	603	22.0	349	18	R5070	Somatostatin-like rec	1.35e-43
33	578	21.1	402	18	R98358	C-C chemokine recepto	3.98e-41
34	569	20.7	355	11	R52749	Mouse pancreas G-prot	2.69e-40
35	563	20.5	348	17	R91229	Mouse pancreas beta-c	9.60e-40
36	563	20.5	348	18	R95069	CC-chemokine receptor	3.05e-35
37	514	18.7	355	15	R48730	G-protein coupled bov	5.74e-35
38	511	18.6	325	16	R48730	G-protein coupled bov	5.74e-35
39	511	18.6	325	19	W02702	Human G-protein recep	2.03e-34
40	505	18.4	355	20	W07618	Seven transmembrane r	1.10e-33
41	497	18.1	389	10	R53750	CC-chemokine receptor	1.57e-33
42	495	18.0	355	18	W03376	CC-chemokine receptor	2.06e-33
43	494	18.0	359	18	R44531	Human angiotensin II	3.14e-33
44	492	17.9	359	9	R44531	Human angiotensin II	3.14e-33
45	479	17.5	363	13	R65934	Mouse AT2 receptor.	4.83e-32

ALIGNMENTS

RESULT 1
ID R67670 standard; Protein; 372 AA.
AC R67670;

DE 17-ADG-1995 (first entry)
DE Mouse delta opiod receptor MOR1.
KW Mouse; Kappa; delta; mu; opiod receptor; brain; primer; PCR; amplify;
KW transmembrane domain; somatostatin; receptor; human; expression vector;
KW truncate; chimeric; assay; probe.
OS Mus musculus.
PN W09428132-A.

PD 08-DEC-1994.
PF 20-MAY-1994; U05747.
PR 20-MAY-1993; US-066296.
PR 30-JUL-1993; US-100694.
PR 05-NOV-1993; US-147592.
PA (ARCH-) ARCH DEV CORP.
PI Bell GI, Resline T, Yasuda K;
PI WPI; 95-022804/03.
DR N-PSDB; Q75927
PT Polynucleotides and peptides derived from opiod receptor
PT polypeptides - for use in therapeutic compositions and in
PT screening assays for useful drug substances.
PS Claim 5; Page 215-221; 300pp; English.
CC The amino acid sequence of the novel mouse delta opiod receptor MOR1.
CC a fragment (amplified from the cDNA library with primers Q75925-30) as a
CC probe. The primers are based on the conserved sequences present in the
CC second and third transmembrane domains of somatostatin (SRIF) receptor
CC subtypes SSTR1, SSTR2 and SSTR3. The 1.3 kb EcoRI-SacI fragment from the
CC mouse delta opiod receptor clone, lambda ms1-2, was subcloned into the
CC PCMV-msl-2 was transfected into COS-1 cells for protein production. The
CC gene encoding the opiod receptor can be used to produce complete.
CC truncated or chimeric opiod receptor proteins. The opiod receptors
CC thus produced are useful for the development of novel assays designed to
CC select or improve substances, capable of interacting with the opiod
CC receptor proteins, for use in diagnosis, drug design and therapeutic
CC applications.
SQ Sequence 372 AA;

Query Match 100.0%; Score 2743; DB 13; Length 372;
Best Local Similarity 100.0%; Pred. No. 3.05e-247;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 relpsaraelqssplvnlsgafpsafpsaganaasgpgarsaaslaialaialysavc 60
 CC |||||
 CC 1 MELVPSARAELQSSPLVNLSDAFPSAPPSAGANASGSGARSASLAIATLALYSAVC 60
 QY
 Db 61 avgl1gnv1vmfgyrvtklktatniyifnlaladalatsl1pfsakymetwfgell 120
 CC |||||
 CC 61 AVGL1GNV1VMFGYRVTKLKTATNIYIFNLADALATSL1PFSAKYMETWFGELL 120
 QY
 Db 121 ckaylsidyvmfcsiftltmsvdryiaavchpykaldfrtpakaklinc1w1aasgvg 180
 CC |||||
 CC 121 CKAYLSIDYVMFCSIFLTMSVDRIYAVCHPYKALDFRTPAKAKLINCIW1AASGVG 180
 QY
 Db 181 vpinmavtqprdgavvcm1qfppswydwtkicvflfa1vwp111tvcyglm1lri 240
 CC |||||
 CC 181 VPIMVAVTQPRDGAIVCM1QFPSPWYDWTKICVFLFAVWP111TVCYGLM1LRL 240
 QY
 Db 241 rsvrllsgskedrs1rrlttmv1vvvgafvvcwaph1hfv1w1v1g1nrrdp1vvaal 300
 CC |||||
 CC 241 RSVRLSSGSKEDRS1RRITRMV1VVGAFVVCWAPH1HFW1W1V1G1NRRDP1VVAAL 300
 QY
 Db 301 hclalgyansl1npv1yaf1denfkrctfrcpqrqepgs1rrpqrattreervtac 360
 CC |||||
 CC 301 HCLALGYANSS1NPV1YAF1DENFKRCFRCQRCRPPCGRQEPGSLRRPQATTREERVAC 360
 QY
 Db 361 tpsdgp9gggaaa 372
 CC |||||
 CC 361 TPSDGP9GGGAAA 372
 QY
 RESULT 2
 ID R48629 standard; Protein: 372 AA.
 AC R48629;
 DT 15-SEP-1994 (first entry)
 DE Sequence of murine delta opioid receptor deduced from the
 DE DOR-1 cDNA clone.
 KW Opioid receptor; morphine; opiate.
 OS Mus musculus.
 FH Key Location/Qualifiers
 FT Region 46..75
 FT /label= putative membrane spanning region
 FT Region 85..102
 FT /label= see above
 FT Region 125..144
 FT /label= see above
 FT Region 168..189
 FT /label= see above
 FT Region 215..238
 FT /label= see above
 FT Region 262..284
 FT /label= see above
 FT Region 295..308
 FT /label= see above
 FT MO94C4552-A.
 PD 03-MAR-1994;
 PD 13-APR-1993; U07665.
 PR 13-APR-1992; US-929200.
 PA (REGC) UNIV CALIFORNIA.
 PI Edwards RH, Evans CJ, Kaufman D, Keith DE;
 DR WPI: 94-083099/10.
 DR N-PSDB; Q56700.
 PT DNA encoding opioid receptors and antibodies against this
 PT receptor - used to express and locate these receptors, and screen
 PT opds. for opioid (ant)agonist activity
 PS clain 10; Fig 5; 74pp; English.
 CC A cDNA library was constructed using mRNA isolated from the NG109-15
 CC cell line. A single clone, named the DOR-1 clone was isolated.
 CC Comparisons with known sequences in GenBank showed highest homology
 CC between DOR-1 and the G-protein-coupled somatostatin receptor. Other
 CC features of the DOR-1 clone AA sequence deduced from the cDNA
 CC sequence include 3 consensus glycosylation sites at residues 18 and
 CC 33 (predicted to be in the extracellular N-terminal domain), and at
 CC residue 310 (close to the C-terminus and predicted to be
 CC intracellular). Phosphokinase C consensus sites are present within

CC predicted intracellular domains, at residues 242,255, 344 & 352.
 CC Seven putative membrane-spanning regions were identified. The DOR-1
 CC clone produces a delta receptor with a predicted mol. wt. of 40,558
 CC kdaltons prior to post-translational modifications.
 SQ Sequence 372 AA;
 Query Match 100.0%; Score 2743; DB 9; Length 372;
 Best Local Similarity 100.0%; Pred. No. 3,05e-247;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 melvpsaraelqssplvnlsgafpsafpsaganaasgpgarsaaslaialaialysavc 60
 CC |||||
 CC 1 MELVPSARAELQSSPLVNLSDAFPSAPPSAGANASGSGARSASLAIATLALYSAVC 60
 QY
 Db 61 avgl1gnv1vmfgyrvtklktatniyifnlaladalatsl1pfsakymetwfgell 120
 CC |||||
 CC 61 AVGL1GNV1VMFGYRVTKLKTATNIYIFNLADALATSL1PFSAKYMETWFGELL 120
 QY
 Db 121 ckaylsidyvmfcsiftltmsvdryiaavchpykaldfrtpakaklinc1w1aasgvg 180
 CC |||||
 CC 121 CKAYLSIDYVMFCSIFLTMSVDRIYAVCHPYKALDFRTPAKAKLINCIW1AASGVG 180
 QY
 Db 181 vpinmavtqprdgavvcm1qfppswydwtkicvflfa1vwp111tvcyglm1lri 240
 CC |||||
 CC 181 VPIMVAVTQPRDGAIVCM1QFPSPWYDWTKICVFLFAVWP111TVCYGLM1LRL 240
 QY
 Db 241 rsvrllsgskedrs1rrlttmv1vvvgafvvcwaph1hfv1w1v1g1nrrdp1vvaal 300
 CC |||||
 CC 241 RSVRLSSGSKEDRS1RRITRMV1VVGAFVVCWAPH1HFW1W1V1G1NRRDP1VVAAL 300
 QY
 Db 301 hclalgyansl1npv1yaf1denfkrctfrcpqrqepgs1rrpqrattreervtac 360
 CC |||||
 CC 301 HCLALGYANSS1NPV1YAF1DENFKRCFRCQRCRPPCGRQEPGSLRRPQATTREERVAC 360
 QY
 Db 361 tpsdgp9gggaaa 372
 CC |||||
 CC 361 TPSDGP9GGGAAA 372
 QY

RESULT 3
 ID R76782 standard; Protein: 372 AA.
 AC R76782;
 DT 11-DEC-1995 (first entry)
 DE Rat delta opiate receptor.
 KW Delta opiate receptor; mu opiate receptor; hMOR; opiate agonist;
 KW opiate antagonist; drug abuse; analgesic.
 OS Rattus sp.
 PN MO9520667-A1.
 PD 03-AUG-1995;
 PD 30-JAN-1995; U01144.
 PR 28-JAN-1994; US-186275.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (USSH) US SEC DEPT HEALTH.
 PI Johnson PS, Persico AM, Dhl G, Wang J;
 DR WPI: 95-275452/36.
 PT New DNA encoding human mu opiate receptor - used esp. for screening
 PT opds. for activity as opiate agonists or antagonists
 PS disclosure; Page 28-29; 49pp; English.
 CC hMOR cDNA was obtd. from a human cerebral cortical cDNA library
 CC screened with fragments of a rat mu opiate receptor. The encoded
 CC protein showed homology to rat mu, delta and kappa opiate
 CC receptors (R76781-83).
 SQ Sequence 372 AA;
 Query Match 96.6%; Score 2650; DB 14; Length 372;
 Best Local Similarity 96.8%; Pred. No. 2.72e-238;
 Matches 360; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
 Db 1 melvpsaraelqssplvnlsgafpsafpsaganaasgpgarsaaslaialaialysavc 60
 CC |||||
 CC 1 MELVPSARAELQSSPLVNLSDAFPSAPPSAGANASGSGARSASLAIATLALYSAVC 60
 QY
 Db 61 avgl1gnv1vmfgyrvtklktatniyifnlaladalatsl1pfsakymetwfgell 120
 CC |||||


```

QY 61 AVGLIGNLVMEGIYRKYKLTATNTIYFNALADALNTSTIPROSAKIMETWPFGEEL 120
DB 121 CKAVLSIDYMMFTSIFILTMSSVDRIYAVCHPVKALDFFIRPAKAKLINICIWLAASVY 180
QY 121 CKAVLSIDYMMFTSIFILTMSSVDRIYAVCHPVKALDFFIRPAKAKLINICIWLAASVY 180
DB 181 VPIMMAVTPGRDGA-VYCMLOFPSPSWMDTVYKICVFLFAFVVPILITVCYGLMLRL 240
QY 181 VPIMMAVTPGRDGA-VYCMLOFPSPSWMDTVYKICVFLFAFVVPILITVCYGLMLRL 240
DB 241 RSVRLISGSKKRSRLRRITRMVLVYVGAFFVCMAPIHIFVITVLDINRDPVVAAL 300
QY 241 RSVRLISGSKKRSRLRRITRMVLVYVGAFFVCMAPIHIFVITVLDINRDPVVAAL 300
DB 301 HLCLALGYANSSLNPFVLAFLDENFKRCFROLCTPCGRQPSGLRRPQATRERYTAC 360
QY 301 HLCLALGYANSSLNPFVLAFLDENFKRCFROLCTPCGRQPSGLRRPQATRERYTAC 360
DB 361 TSPSGPGGGA 372
QY 361 TSPSGPGGGA 372

```

```

RESULT 4
ID R66503 standard; Protein; 371 AA.
AC R66503;
DT 19-JAN-1995 (first entry)
DE Murine delta opioid receptor.
KW delta opioid; enkephalin; receptor; mouse; murine; analgesic; pain;
KW drug addiction; neurological disorder; psychiatric; disorder;
KW cardiovascular disorder.
OS Mus musculus.
PN FR6697850-A.
PD 13-MAY-1994.
PF 10-NOV-1992; 013526.
PR 10-NOV-1992; FR-013526.
PA (UYST-) UNITV PASTEUR STRASBOURG LOUIS.
PI Kieffer B;
DR WPI: 94-117825/22.
DR N-PSDB: Q66656.
PT New nucleic acid encoding opioid receptor - and related
PT polypeptide, antisense nucleic acid, probes, recombinant cells
PT and ligands, useful in diagnosis and treatment of e.g.
PT neurological disorders
PS Claim 8; Page 19-20; 29pp; French.
CC A cDNA bank constructed from hybridoma NG108-15, was used to
CC transfect COS-1 cells. The cells were tested for ability to bind
CC tritium-labelled Tyr-D-Thr-Gly-Phe-Leu-Thr, in the presence or
CC absence of the opioid antagonist naloxone. Clone K56 was isolated
CC from a positive colony and found to contain a 2210bp insert. This
CC cDNA encodes a delta opioid (enkephalin) receptor with apparent
CC dissociation constant 1.4nM and Bmax 3.9-6.4 pmole/mg protein.
SQ Sequence 371 AA;

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Query Match 91.8%; Score 2519; DB 10; Length 371;
Best Local Similarity 95.2%; Pred. No. 1,08e-225;
Matches 355; Conservative 0; Mismatches 15; Indels 3; Gaps 3;

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DB 1 MEIYPSARAEIQSSPLVNLSDAFPAFSAQANASGSPGARASALLAIALTALYSAVC 60
QY 1 MEIYPSARAEIQSSPLVNLSDAFPAFSAQANASGSPGARASALLAIALTALYSAVC 60
DB 61 AVGLIGNLVMEGIYRKYKLTATNTIYFNALADALNTSTIPROSAKIMETWPFGEEL 120
QY 61 AVGLIGNLVMEGIYRKYKLTATNTIYFNALADALNTSTIPROSAKIMETWPFGEEL 120
DB 121 CKAVLSIDYMMFTSIFILTMSSVDRIYAVCHPVKALDFFIRPAKAKLINICIWLAASVY 180
QY 121 CKAVLSIDYMMFTSIFILTMSSVDRIYAVCHPVKALDFFIRPAKAKLINICIWLAASVY 180
DB 181 VPIMMAVTPGRDGA-VYCMLOFPSPSWMDTVYKICVFLFAFVVPILITVCYGLMLRL 238
QY 181 VPIMMAVTPGRDGA-VYCMLOFPSPSWMDTVYKICVFLFAFVVPILITVCYGLMLRL 238

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QY 181 VPIMMAVTPGRDGA-VYCMLOFPSPSWMDTVYKICVFLFAFVVPILITVCYGLMLRL 239
DB 239 IISVRLISGSKKRSRLRRITRMVLVYVGAFFVCMAPIHIFVITVLDINRDPVVAAL 298
QY 240 RSVRLISGSKKRSRLRRITRMVLVYVGAFFVCMAPIHIFVITVLDINRDPVVAAL 299
DB 299 HLCLALGYANSSLNPFVLAFLDENFKRCFROLCTPCGRQPSGLRRPQATRERYTAC 358
QY 300 HLCLALGYANSSLNPFVLAFLDENFKRCFROLCTPCGRQPSGLRRPQATRERYTAC 359
DB 359 CTSPSGPGGGA 371
QY 360 CTSPSGPGGGA 372

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RESULT 5
ID R6780 standard; Protein; 400 AA.
AC R6780;
DT 11-DEC-1995 (first entry)
DE Human mu opiate receptor.
KW Human mu opiate receptor; hMOR; opiate agonist; opiate antagonist;
KW drug abuse; analgesic.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Modified site 9
FT /label= Glycosylation
FT /note= "N-linked glycosylation site"
FT Modified site 11
FT /label= Glycosylation
FT /note= "N-linked glycosylation site"
FT Modified site 32
FT /label= Glycosylation
FT /note= "N-linked glycosylation site"
FT Modified site 40
FT /label= Glycosylation
FT /note= "N-linked glycosylation site"
FT Modified site 48
FT /label= Glycosylation
FT /note= "N-linked glycosylation"
FT Domain 68..87
FT /label= Transmembrane_domain
FT Domain 107..125
FT /label= Transmembrane_domain
FT Domain 144..165
FT /label= Transmembrane_domain
FT Domain 188..208
FT /label= Transmembrane_domain
FT Domain 236..256
FT /label= Transmembrane_domain
FT Domain 284..304
FT /label= Transmembrane_domain
FT Domain 322..341
FT /label= Transmembrane_domain
FT Domain 359..371
FT /label= Transmembrane_domain
EN WO9520667-A1.
PD 03-AUG-1995.
PF 30-JAN-1995; U01144.
PR 28-JAN-1994; US-188275.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (USSH ) US SEC DEPT HEALTH.
PI Johnson PS, Persico AM, Uhl G, Wang J;
DR WPI: 95-275452/36.
DR N-PSDB: Q93102.
PT New DNA encoding human mu opiate receptor - used esp. for screening
PT cpls. for activity as opiate agonists or antagonists
PS Claim 1; Page 25-26; 49pp; English.
CC hMOR cDNA was obt'd. from a human cerebral cortical cDNA library
CC screened with fragments of a rat mu opiate receptor. Expression
CC of hMOR1 in COS cells revealed high affinity recognition of the mu
CC opiate specific ligand. Recombinant hMOR1 can be used to screen
CC compounds for analgesic activity.
SQ Sequence 400 AA;

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Query Match 63.0%; Score 1729; DB 14; Length 400;

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	Best Local Similarity	64.3%	Pred No. 6,41e-150:	
	Matches	220:	Conservative	58: Mismatches 61: Indels 3: Gaps 3:
Dd	40	rlsdpogpurtlnlgardslcpt-gspsmittaitlmalyisivecvvglfngflvmtyivry	98	
Qy	18	nlldafpsapsagannasgspgarsasstlmlatlmlyavavagllgvlwefgvr	77	
Dd	99	tkaktatnifflaladalatatgtpfgsvrylmgtwpgftgllolklvisldyymftsif	158	
Qy	78	cktktatnntienmladlalatstltpfqsakylmetmpfbedlckatlsldyymfssif	137	
Dd	159	tlctmsvdyriavchpykalditfrpnaki:inyovnwllsaisiglpymfmatktyrgsid	218	
Qy	138	tlmmvsvdriavchpkaadfrfprapaklnticowllasgavp iwmvavtpordavv	197	
Dd	219	ctltfssprtywaelvykvcyfifafimrvllitvcyglmlrlksvmlsgskednrlr	278	
Qy	198	cmlofpepsmtdvwtatlcovflfevvpillitvtycgmllrlksvayllssskkdsrlr	257	
Dd	279	rtttmrvlwyavavifcwtbphihlylkalvli-pettftqvswfhciajlytmsclnrvl	337	
Qy	258	rttfmrvlwyavavfvcwaphifhifvmtlvdinrddpvlvvaalrhcialtgsnslrvpl	317	
Dd	338	yafidenfkrctfrcfipstns:ieqgnsrlrgrnt-rdhpst	378	
Qy	318	yafidenfkrctfrcfipstns:ieqgnsrlrgrnt-rdhpst	359	

SEQ	RESULT	6
ID	R71966	standard; Protein; 400 AA.
AC	R71966;	
DE	20-OCN-1995 (first entry)	
DI	Human mu opioid receptor.	
KW	Mu opioid receptor; MOR; gene therapy; diagnostic.	
OS	Homo sapiens.	
PN	W09507983-A.	
PD	23-MAR-1995.	
PF	13-SEP-1994; U10358.	
PR	13-SEP-1993; US-120601.	
PA	(INDV) UNIV INDIANA FOUND.	
PI	Yu L;	
DR	WPI; 95-131351/17.	
DR	N-ESTD; Q899226.	
PT	New nucleic acid encoding new human mu opioid receptor - and	
PT	related vectors, transformed cells, antibodies etc., useful in	
PT	diagnosis, treatment and drug screening.	
PS	Claim 4; Page 211-214; 265pp; English.	
CC	A cDNA library constructed from human caudate nucleus mRNA was	
CC	screened with rat mu opioid receptor cDNA under conditions of	
CC	low stringency. One positive clone included the sequence given	
CC	in	
CC	Q89226, encoding a mu opioid receptor MOR (R71966). The cDNA	
CC	is used for produ. of recombinant MOR, in gene therapy, etc.	
CC	Sequence 400 AA;	

Query Match	62.9%;	Score 1725;	DB 13;	Length 400;
Best Local Similarity	64.3%;	Pred. No. 1.55e-149;		
Matches 720;	Conservative 57;	Mismatches 62;	Indels 3;	Gaps 3;

[illegible]

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D6      279   ritmrvlwwavvifvcwtpihyivlikalvtl-pettfgtswhfialgynslnpyl 337  
          |||||:::|||::|::|::|::|::|::|::|::|::|::|::|::|:  
QY      258 RITRMVLVWGAVVGAWCAPIHIFIVILTWLDINDIRDDPLVAALHICIAIGYNSSLNPYL 317  
  
Db       338 yaflidenfrcfcfrfcrlptsmldegqnstlrnt-ridpst 378  
          |||||:::|||::|::|::|::|::|::|::|::|::|::|:  
QY       318 YAFLEDNFKRCFROLCRTGCGROEPGSLLRRPRKATTRERYTA 359  
  
RESULT           7  
ID      R71964 standard; protein; 398 AA.  
AC      R71964;  
DT      20-OCT-1995 (first entry)  
DE      Rat mu opioid receptor.  
KW      Mu opioid receptor; MOR-1; gene therapy; diagnostic.  
OS      Rattus sp.  
PN      W09507983-A.  
PD      23-MAR-1995.  
PF      13-SEP-1994; U10358.  
PI      PR 13-SEP-1993; US-120601.  
PA      ( INDV ) UNIV INDIANA FOUND.  
PY      Yu L;  
DR      WPJ: 95-11351/17.  
DS      N-PESDB; Q89222  
PT      New nucleic acid encoding new human mu opioid receptor - and  
PT      related vectors, transformed cells, antibodies etc., useful in  
PT      diagnosis, treatment and drug screening.  
PS      Disclosure; Page 190-194; 266bp; English.  
CC      A 365 bp fragment of the mouse delta opioid receptor was used to  
CC      screen a rat brain cDNA library under low stringency conditions.  
CC      One positive clone included the sequence given in Q89222, encoding a  
CC      mu opioid receptor, MOR-1 (R71964). MOR-1 was stably expressed in  
CC      transfected CHO cells.  
SQ      Sequence 398 AA;
```

Query Match	62.8%;	Score 1723;	DB 13;	Length 398;
Best Local Similarity	66.08;	Pred. No. 2,40e-149;		
Matches 217;	Conservative 55;	Mismatches 54;	Indels 3;	Gaps 3;

[illegible]

RESULT	8
ID	RS5188 standard; Protein: 356 AA.
AC	RS5188;
DT	19-APR-1995 (fixat entry)
DE	Murine mu-subtype opioid receptor.
KW	Mu-subtype opioid receptor; MOR; drug addiction
OS	Rattus rattus.
PR	Key Location/Qualifiers

FT Modified site 10..12
 FT /note= "Putative N-linked glycosylation site"
 FT Modified site 230
 FT /note= "Threonine residue especially favourable
 FT for protein kinase A phosphorylation"
 FT Region 25..48
 FT /note= "hydrophobic membrane spanning region"
 FT Region 58..78
 FT /note= "hydrophobic membrane spanning region"
 FT Region 96..118
 FT /note= "hydrophobic membrane spanning region"
 FT Region 139..166
 FT /note= "hydrophobic membrane spanning region"
 FT Region 187..212
 FT /note= "hydrophobic membrane spanning region"
 FT Region 236..257
 FT /note= "hydrophobic membrane spanning region"
 FT Region 274..294
 FT /note= "hydrophobic membrane spanning region"
 PN EP-612845-A.
 PD 31-AUG-1994.
 PF 09-FEB-1994; 101968.
 PR 26-FEB-1993; US-026140.
 PA (AMCY) AMERICAN CYANAMID CO.
 PI Corbett M.J., Eppler CM., Shieh H., Zysk JR;
 DR WPI; 94-265963/33.
 DR N-PSDB; Q79199.
 PT Pure mu-type opioid receptor protein - and nucleic acid coding
 PT for it
 PS Claim 2; Fig 9; 39pp; English.
 CC R65188 is the rat mu-subtype opioid receptor protein purified
 CC from rat brain membranes, with biotinyl-b-endorphin (856666)
 CC as its ligand. It is encoded by the nucleotide sequence Q79199
 CC R65188 is synthesised using Q71022 and Q71023 as PCR primers.
 CC screening new opioid ligands, and for studying mechanisms of
 CC opioid action, e.g. drug addiction.
 SQ Sequence 356 AA;

Query Match 62.7%; Score 1721; DB 11; Length 356;
 Best Local Similarity 65.7%; Pred. No. 3.73e-149;
 Matches 216; Conservative 56; Mismatches 54; Indels 3; Gaps 3;

Dh 9 ggnndslcpqt-gspsmvtaittmalysivcvgylfgnflmwyivrytkmktatniyifn 67
 QY 31 GANASGSPGARSSALALATITATISAVCAVGLGNVLMVGIVRYTKLKTATNIYIFN 90
 Dh 68 laladaltstlpfgsvnylmgtwptfgtlckivlsidgymftsiflctmsvdriay 127
 QY 91 LALADALATSTLPFGSAKYIMETWPEGLCKAVLSIDYNNFTSIFTLTKMSVDRIAY 150
 Dh 128 chpykaldfrprnakivncvnlssalgipvmfmatkkyrgsidctltfshptwyw 187
 QY 151 CHPYKALDFRPAKAKLTINICIMVILASGVGVPIMVAVTQPRDAGVWCVLQFPSPSWMD 210
 Dh 188 nlkicvffafimpylittvcyglmrlrksvmlsgskednrlritmnylvvavf 247
 QY 211 TVTKICVLEFAFVPIILITVYCGMLRLRSVRLSSKSKEDSLRITRMVAVVGA 270
 Dh 248 lvcwtpghlylkalitl-pettfgtvswhfcalagytusclnrvlyafidenfkrcfr 306
 QY 271 VCVWAPHIHFIVTWLVINRDRPLVVAALHCLIALGVANSINPVLYAFIDENFKRCFR 330
 Dh 307 efcldptstieqgnsttryqnt-rehps 334
 QY 331 QLCRTPCGRQEPGSLRRPRQATTRERYTA 359

RESULT 9
 ID R76781 standard; Protein; 398 AA.
 AC R76781;
 DT 11-DEC-1995 (first entry)
 DE Rat mu opiate receptor.

KM Mu opiate receptor; hMOR; opiate agonist; opiate antagonist;
 KW drug abuse; analgesic.
 OS Rattus sp.
 PN MO9520657-A1.
 PD 03-AUG-1995.
 PF 30-JAN-1995; T01144.
 PR 28-JAN-1994; US-188275.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI (USSH) US SEC DEPT HEALTH.
 DR Johnson PS. Persico AM, Uhl G, Wang J;
 DR WPI; 95-275452/36.
 PT New DNA encoding human mu opiate receptor - used esp. for screening
 PT opds. for activity as opiate agonists or antagonists
 PS Disclosure; Page 26-28; 49pp; English.
 CC hMOR cDNA was obtd. from a human cerebral cortical cDNA library
 CC screened with fragments of a rat mu opiate receptor. The encoded
 CC protein showed homology to rat mu, delta and kappa opiate
 CC receptors (R76781-83).
 SQ Sequence 398 AA;

Query Match 62.7%; Score 1721; DB 14; Length 398;
 Best Local Similarity 65.7%; Pred. No. 3.73e-149;
 Matches 216; Conservative 56; Mismatches 54; Indels 3; Gaps 3;

Dh 51 ggnndslcpqt-gspsmvtaittmalysivcvgylfgnflmwyivrytkmktatniyifn 109
 QY 31 GANASGSPGARSSALALATITATISAVCAVGLGNVLMVGIVRYTKLKTATNIYIFN 90
 Dh 110 laladaltstlpfgsvnylmgtwptfgtlckivlsidgymftsiflctmsvdriay 169
 QY 91 LALADALATSTLPFGSAKYIMETWPEGLCKAVLSIDYNNFTSIFTLTKMSVDRIAY 150
 Dh 170 chpykaldfrprnakivncvnlssalgipvmfmatkkyrgsidctltfshptwyw 229
 QY 151 CHPYKALDFRPAKAKLTINICIMVILASGVGVPIMVAVTQPRDAGVWCVLQFPSPSWMD 210
 Dh 230 nlkicvffafimpylittvcyglmrlrksvmlsgskednrlritmnylvvavf 289
 QY 211 TVTKICVLEFAFVPIILITVYCGMLRLRSVRLSSKSKEDSLRITRMVAVVGA 270
 Dh 290 lvcwtpghlylkalitl-pettfgtvswhfcalagytusclnrvlyafidenfkrcfr 348
 QY 271 VCVWAPHIHFIVTWLVINRDRPLVVAALHCLIALGVANSINPVLYAFIDENFKRCFR 330
 Dh 349 efcldptstieqgnsttryqnt-rehps 376
 QY 331 QLCRTPCGRQEPGSLRRPRQATTRERYTA 359

RESULT 10
 ID R72591 standard; Protein; 380 AA.
 AC R72591;
 DT 01-DEC-1995 (first entry)
 DE Mammalian kappa opiate receptor protein.
 KW Mammalian kappa opiate receptor; mouse delta opiate receptor; analgesic;
 KW amplification; primer; rat; probe; E.coli; RT-PCR; hypnotic compound; ds.
 OS Rattus rattus.
 FH Key
 FT CDS Location/Qualifiers
 FT /tag= a
 FT /product= kappa opiate receptor
 PN J07070191-A.
 PD 14-MAR-1995.
 PF 30-JUL-1993; 190261.
 PR 09-JUL-1993; UP-170591.
 PA (TAKE) TAKEEDA CHEM IND LTD.
 DR WPI; 95-144857/19.
 DR N-PSDB; Q86725.
 PT kappa opiate receptor protein and cells expressing it - useful
 PT for the screening of compounds for analgesic and hypnotic
 PT properties
 PS Claim 2; Page 9-10; 15pp; Japanese.
 CC The amino acid sequence of the novel mammalian kappa opiate receptor.

CC The gene was isolated by amplifying a fragment from rat brain mRNA by
 CC reverse transcriptase-PCR (RT-PCR) using primers 086726-7 derived from
 CC the mouse delta-opioid receptor gene. This fragment was cloned into the
 CC plasmid pCR1 to produce pR1. The plasmid pR1 was used to probe a rat
 CC brain DNA library in lambda ZAPII to obtain a clone of the rat kappa
 CC opioid receptor gene, designated pKOR. This clone was introduced into
 CC E.coli JM109 for production of the receptor protein. The receptor protein
 CC is useful for screening of analgesic and hypnotic compounds including
 CC peptides and proteins.
 SQ Sequence 380 AA;

Query Match 58.5%; Score 1604; DB 14; Length 380;
 Best Local Similarity 67.0%; Pred. No. 5,63e-138;
 Matches 207; Conservative 51; Mismatches 45; Indels 6; Gaps 5;

DB 57 aipvliiaavsvvrvvglymglmslwmfvlirytkmktatniyifnlaladalavttmfpqs 116
 QY 47 ALAIAITATLISAVCAVGLGNVLMFGLVIRYTKTKTATNTITFNLALADALATSTLPPQS 106
 DB 117 avylmswpgfdvrlckivisldyymftsifltlmsvdrlyavchpvcakldftrplkak 176
 QY 107 AKYLMETWPEGLCKAVSLIDYNNFTSIFTLTMSVDRIYAVCHPVALDRIETPAKAK 166
 DB 177 llniclwllasvgsiaalygqtkvredvdlscslqfpddegsw-wdlfmkicvtfaf 235
 QY 167 LINCIMWLASGVGVPIMVAVQPRDGA-VV-CMLQFPSP--SWWDTVTIKICVLFPAF 222
 DB 236 vlpvliiivcylmlrlkavrllsgsrekdnrlrrtklrvvvavfllcwtpihifil 295
 QY 223 VPIILITVCGMLRLRSVRLLSGSKEDRSILRRITRMVLYVVGAVVCGAPRIHIFVI 282
 DB 296 vealgstshsta-vlsayfcialqyunslnpylyafldenfkrcifdcfpikmmer 354
 QY 283 VWTLVDINRDPPIVVAALHICINALGVANSSLPVLYAFDENFKRCFOLCRTPCGRQEP 342
 DB 355 qstnrvnt 363
 QY 343 GSLRRPPOA 351

RESULT 11
 ID R76783 standard; Protein; 380 AA.
 AC R76783;
 DT 11-DEC-1995 (first entry)
 DE Rat kappa opiate receptor.
 KW kappa opiate receptor; mu opiate receptor; hMOR; opiate agonist;
 KW opiate antagonist; drug abuse; analgesic.
 OS Rattus sp.
 PN W09520667-A1.
 PD 03-AUG-1995.
 PF 30-JAN-1995; U01144.
 PR 28-JAN-1994; US-188275.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI (USSH) US SEC DEPT HEALTH.
 PI Johnson PS; Persico AM; Uhl G; Wang U;
 DR WPI; 93-275432/36.
 PT New DNA encoding human mu opiate receptor - used esp. for screening
 PT cpds. for activity as opiate agonists or antagonists
 PS Disclosure; Page 29-30; 49pp; English.
 CC hMOR cDNA was obt'd. from a human cerebral cortical cDNA library
 CC screened with fragments of a rat mu opiate receptor. The encoded
 CC protein showed homology to rat mu, delta and kappa opiate
 CC receptors (R76781-83).
 SQ Sequence 380 AA;

Query Match 58.5%; Score 1604; DB 14; Length 380;
 Best Local Similarity 67.0%; Pred. No. 5,63e-138;
 Matches 207; Conservative 51; Mismatches 45; Indels 6; Gaps 5;

DB 57 aipvliiaavsvvrvvglymglmslwmfvlirytkmktatniyifnlaladalavttmfpqs 116
 QY 47 ALAIAITATLISAVCAVGLGNVLMFGLVIRYTKTKTATNTITFNLALADALATSTLPPQS 106

DB 117 avylmswpgfdvrlckivisldyymftsifltlmsvdrlyavchpvcakldftrplkak 176
 QY 107 AKYLMETWPEGLCKAVSLIDYNNFTSIFTLTMSVDRIYAVCHPVALDRIETPAKAK 166
 DB 177 llniclwllasvgsiaalygqtkvredvdlscslqfpddegsw-wdlfmkicvtfaf 235
 QY 167 LINCIMWLASGVGVPIMVAVQPRDGA-VV-CMLQFPSP--SWWDTVTIKICVLFPAF 222
 DB 236 vlpvliiivcylmlrlkavrllsgsrekdnrlrrtklrvvvavfllcwtpihifil 295
 QY 223 VPIILITVCGMLRLRSVRLLSGSKEDRSILRRITRMVLYVVGAVVCGAPRIHIFVI 282
 DB 296 vealgstshsta-vlsayfcialqyunslnpylyafldenfkrcifdcfpikmmer 354
 QY 283 VWTLVDINRDPPIVVAALHICINALGVANSSLPVLYAFDENFKRCFOLCRTPCGRQEP 342
 DB 355 qstnrvnt 363
 QY 343 GSLRRPPOA 351

RESULT 12
 ID R88722 standard; Protein; 380 AA.
 AC R88722;
 DT 04-SEP-1996 (first entry)
 DE Human kappa opioid receptor.
 KW Human; kappa opioid receptor; psychiatric disorder; cardiovascular;
 KW neurology; diagnosis.
 OS Homo sapiens.
 PN W09601898-A1.
 PD 25-JAN-1996.
 PF 07-JUL-1995; F00912.
 PR 11-JUL-1994; FR-008531.
 PA (URST-) UNIT PASTEUR STRASBOURG LOUIS.
 PI Kieffer B; Simonin F;
 DR WPI; 96-097628/10.
 DR N-PSDB; 112550.
 PT New nucleic acid encoding the human Kappa opioid receptor - useful
 PT in diagnosis and therapy, and for isolating receptor ligands and
 PT modulators
 PS Claim 7; Page 13-15; 30pp; French.
 CC The sequence coding for the human kappa opioid receptor was
 CC obtained from two overlapping cDNA fragments isolated from a
 CC human placental cDNA library. The fragments were amplified from
 CC the library using PCR primers based on the sequence of human
 CC genomic clones which hybridised with a murine delta receptor cDNA
 CC probe. Nucleotide probes derived from the kappa opioid receptor
 CC coding sequence are useful for diagnosis of neurological, cardio-
 CC vascular and psychiatric disorders associated with opioid
 CC receptors. The receptor can be used for identifying e.g. agonists
 CC of its activity for potential use as analgesics.
 SQ Sequence 380 AA;

Query Match 58.5%; Score 1604; DB 17; Length 380;
 Best Local Similarity 63.6%; Pred. No. 5,63e-138;
 Matches 213; Conservative 56; Mismatches 59; Indels 7; Gaps 7;

DB 30 fpgwaepdngsgsedqdephlspaijvliitavsvrvvglymglmslwmfvliryt 89
 QY 23 FPS-APP-PAGANASGSPGARSAS-SLALAIAITATLISAVCAVGLGNVLMFGLVIRYTK 79
 DB 90 mktatniyifnlaladalavttmfpqstvylnmswpgfdvrlckivisldyymftsifcl 149
 QY 80 LKTAITNTITFNLALADALATSTLPPQSARKIMTWPEGLCKAVSLIDYNNFTSIFTL 139
 DB 150 tmsvdrlyavchpvcakldftrplkaklilniclwllasvgsiaalygqtkvredvdl 209
 QY 140 TMSVDRIYAVCHPVALDRIETPAKAKLINCIMWLASGVGVPIMVAVQPRDGA-VV- 197
 DB 210 csqfddddswdlfmkicvtfafylyvllivcylmlrlkavrllsgsrekdnrl 269
 QY 198 CMLQFPSPSW-WMDVTIKICVLFPAFVPIILITVCGMLRLRSVRLLSGSKEDRSIL 256

Dbb 57 aadlhtayrsyrfvvgvlagnstvmfvilrtyckmkcatnlyfnaladaalyttmfigs 116
|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||
47 AIAAIAITAKSAACAAGLLGNVLMWFGIVRYKTKATNTATNYIFNIALALAPALTSTLPEFS 106

Ddb 117 avylmswdfgdvalckivisldgymftsifcltmsvgrilyavchpykaldftrlpak 176
| | | | | : : : : : |||:::|||:::|||:::|||:::|||:::|||:::|||:::|||
107 AYIMEIWEFEGELCKAVISIDYNNFTSIFLTLMMSVDRIYAVCHPYKALDFRTPARK 166

Ddb 117 annicwlassvgsaisalggtkrwedvdleostqfddexsw-wdlfmkicvfiaf 235
| | | | | : : : : : |||:::|||:::|||:::|||:::|||:::|||:::|||:::|||
167 LINCICWLASGVGFIMMAVTQPDGA-VV-CMQLPSP--SWMYDWIVTICVLFMF 222

Ddb 236 vdpvllivcytlmlrlrksvrlsgsteekdnlrirkliyvvavaficwtplhifa1 295
| | | | | : : : : : |||:::|||:::|||:::|||:::|||:::|||:::|||:::|||
223 VPIIIIRVCYGLMLRLRSVRLLSGSKERDSLRRTBMVLVVGAFPVCCAPRHIEVI 282

Ddb 236 vealgstshsta-alsxyxfciaigtntslmpvyafidcfrctfdcfcpkimmer 354
| | | : : : : : |||:::|||:::|||:::|||:::|||:::|||:::|||:::|||
283 VMTLVDIRRDVLVVAALHLCIALTGTAANSLNPVYIAFDENEFKKCFQOLCTPGCRDP 342

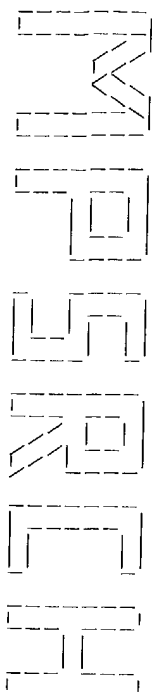
17-AUG-1995 (first entry)
Mouse oploid receptor-like
Mouse; kappa, delta; mu; oploid receptor; brain; primer; PCR; amplify;
transmembrane domain; somatostatin receptor; human; expression vector;
truncate; chimeric; assay; probe.
Mus musculus.
M09428132-A.
08-DEC-1994.
20-MAY-1994; U05747.

PR 20-MAY-1993; US-066296.
 PR 30-JUL-1993; US-100694.
 PR 05-NOV-1993; US-147592.
 PA (ARCH-) ARCH DEV CORP.
 PI Bell GI, Reisine T, Yasuda K;
 DR WPI; 95-022804/03.
 DR N-PSDH; 075928.
 PT Polynucleotides and peptides derived from opioid receptor
 PT polypeptides - for use in therapeutic compositions and in
 PT screening assays for useful drug substances.
 PS Claim 27; Page 225-229; 300pp; English.
 CC The amino acid sequence of the novel mouse opioid receptor-like receptor
 CC MOP2. MOP2 is a mouse receptor with pharmacological properties which
 CC are dissimilar to the properties of classic opioid receptors such kappa,
 CC delta, mu or sigma. It has been found that drugs of high abuse potential
 CC or analgesic potency bind selectively to this receptor. This suggests
 CC that this receptor could be important in the development of drugs to
 CC treat addiction. Other opioid receptors isolated and produced such as the
 CC novel mouse kappa and delta opioid receptors (Q75926-7) are useful for
 CC the development of novel assays designed to select or improve substances,
 CC capable of interacting with the opioid receptor proteins, for use in
 CC diagnosis, drug design and therapeutic applications.
 SO Sequence 367 AA;

Query Match 53.2%; Score 1460; DB 13; Length 367;
 Best Local Similarity 56.3%; Pred. No. 3,07e-124;
 Matches 180; Conservative 67; Mismatches 71; Indels 2; Gaps 2;

Db	44	p g l v t t v g l a v c l g l g n c l m v v l p h t k m k a t n i y f n l a l a d l v l t p f	103
QY	45	S L A I A I A T A L S A V C A V G L S N V L M E G I V Y T K I K T A T N I Y I N L A D A L A T S T P F	104
Db	104	g t d l l g f w f g n a l c t v a l d y n m f t s f l t m s v d y v a l c p l z a l d v t s k	163
QY	105	Q S A K Y L M E W P E G E L C K A V L S I D Y N M P T S I F T L M S V D R Y I A V C H P V K A L D E R T P A K	164
Db	164	a q a v v a l a s v v g v p a l m s g v e e e c l v e l p a q d y g p v f a c l f f s f i	223
QY	165	A K I N I C I W L S G V G P I M V M A V T Q P R D G A V C M Q P S P S W D I V T K I C V L F A E V V	224
Db	224	p l l s v c y s l m r r l g y l l s g r e k d m r r r l v l v v a v f v g c w p v g f v l v q	283
QY	225	P I I I V C I G L M L R K S V K L S G S K E K R S R R R R M V L V V G A V V C M A P H R I V I W	284
Db	284	g l -g v g s e t a v a l r f c t a l g y v n s c l m p i l y a f d e n f k a c f r k f c a s a l h e m g v	342
QY	285	T V D I R R R D I V V A A H L C I A L G A N S L N P Y A F L D E F K C F R Q L C R T P C G R O E P G S	344
Db	343	s d v r -s l a k d v l g c t s e	361
QY	345	L R R R Q A I R R E R V T A C T P S D	364

Search completed: Tue Aug 26 14:44:55 1997
 Job time : 22 secs.



(TM)

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MSEARCH protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jul 18 08:10:10 1997; Maspar time 23.58 Seconds

Tabular output not generated. 291.549 Million cell updates/sec

Title: >US-08-700-356-1
Description: (1-631) from US08700356.pep
Perfect Score: 4516
Sequence: 1 APTATVSGQTRGLIGCITTS.....THPTKYKMGMSADLEVVT 631

Scoring table: PAM 150
Gap 11

Searched: 92623 seqs, 10896596 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq26

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19

Statistics: Mean 36.461; Variance 150.473; scale 0.242

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	4516	100.0	3010	4 R20111	Non-A, non-B viral ge	0.00e+00
2	4516	100.0	3010	4 R20091	Non-A, non-B viral ge	0.00e+00
3	4490	99.4	631	15 R82854	NS3 serine protease d	0.00e+00
4	4407	97.6	2354	8 R41435	PT-NANBH virus non-st	0.00e+00
5	4404	97.5	3014	10 R54093	NANBHV EI/E2 protein.	0.00e+00
6	4397	97.4	3014	7 R35207	Hepatitis C virus pro	0.00e+00
7	4389	97.2	916	18 R82693	HCV partial proteins	0.00e+00
8	4389	97.2	3010	18 R82694	Partial HCV non-struct	0.00e+00
9	4383	97.1	3010	14 R88864	Hepatitis C virus RNA	0.00e+00
10	4377	96.9	3010	13 R86862	HCV protein cleavable	0.00e+00
11	4359	96.5	923	18 R82696	HCV partial proteins	0.00e+00
12	4359	96.5	3010	10 R53417	Blood transmissible N	0.00e+00
13	4337	95.0	3010	7 R24580	Human hepatitis C vir	0.00e+00
14	4327	95.8	2510	6 R29527	HCV antigen T7N1-30.	0.00e+00
15	4328	95.8	3011	8 R40120	HCV genomic amino aci	0.00e+00
16	4325	95.7	2261	12 R66995	Hepatitis C virus gen	0.00e+00
17	4322	95.7	2261	11 R90164	Peptide encoded by gen	0.00e+00
18	4321	95.7	2301	1 P92047	Sequence encoded in t	0.00e+00
19	4322	95.7	2436	1 P92050	Sequence encoded in t	0.00e+00
20	4322	95.7	2462	1 P90288	Peptide encoded by co	0.00e+00

21	4324	95.7	3011	7 R34468	Encoded by full-length	0.00e+00
22	4322	95.7	3011	16 R90931	Hepatitis C virus pol	0.00e+00
23	4316	95.6	1188	6 R29870	HCV NS2-NS4 peptide M	0.00e+00
24	4319	95.6	2772	2 R08123	Hepatitis C virus pol	0.00e+00
25	4315	95.5	1766	1 P90158	Protein sequence of h	0.00e+00
26	4307	95.4	2435	5 R25135	HCV polypeptide 1.	0.00e+00
27	4309	95.4	3011	6 R31621	Hepatitis C virus (HC	0.00e+00
28	4308	95.4	3011	4 R21519	Compiled HCV sequence	0.00e+00
29	4306	95.3	3010	6 R30616	Polypeptide coded by	0.00e+00
30	4300	95.2	2436	5 R28582	HCV amino acid sequen	0.00e+00
31	4301	95.2	3011	8 R40119	HCV genomic amino aci	0.00e+00
32	4301	95.2	3011	14 R79232	HCV sequence.	0.00e+00
33	4296	95.1	2894	13 R70230	Composite hepatitis C	0.00e+00
34	4289	95.0	1766	1 R92041	Sequence encoded in t	0.00e+00
35	4292	95.0	2816	7 P92041	HCV-1 polypeptide.	0.00e+00
36	4285	95.0	2894	5 R24409	Composite HCV HC-J1/C	0.00e+00
37	4283	94.8	2955	2 R24440	Hepatitis C virus put	0.00e+00
38	4262	94.4	3011	4 R22154	NANBH virus c59 isola	0.00e+00
39	4258	94.3	1687	14 R79223	PHCV150-encoded seque	0.00e+00
40	4258	94.3	3011	4 R79223	PHCV176-encoded seque	0.00e+00
41	4251	94.1	1188	6 R29660	HCV NS2-NS4 peptide M	0.00e+00
42	4251	94.1	3011	13 R67588	Hepatitis C virus gen	0.00e+00
43	4116	91.1	840	3 R66267	Hepatitis C virus (HC	0.00e+00
44	4116	91.1	840	3 R14349	Hepatitis C protease::NSD le	0.00e+00
45	4116	91.1	841	13 R68547	HCV protease/NSD fus	0.00e+00

ALIGNMENTS

RESULT 1
ID R20111 standard; Protein; 3010 AA.
AC R20111;

DE 01-MAY-1992 (first entry)
DT Non-A, non-B viral genome product.

KM NANBV; vaccine; immunodiagnosis; antigen: antibody.
OS Non-A, non-B hepatitis virus.

FH Key Location/Qualifiers
FT Protein 1..115

FT /label= C
FT /note= "core protein"

FT /label= M
FT /note= "matrix protein"

FT /label= B
FT /note= "envelope protein"

FT /label= NS1
FT /label= NS2

FT /label= NS3
FT /label= NS4a

FT /label= NS4b
FT /label= NS5

FT /label= NS5
FT /label= NS5

FT /label= NS5
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FT /label= NS5

diagnostics and screening agents for NANBV, and to remove NANBV from

PR blood.
 PS Disclosure: Fig 2; 89pp; English.
 CC The sequence (SEQ ID NO 1) was deduced from several overlapping
 CC "BK" cDNA clones obtd. by "gene walking" using a cDNA clone isolated
 CC from a library prepd. from NANBV RNA. Antigenic polypeptides from
 CC the sequence can be used as immunogens for vaccine prodn. Antibodies
 CC raised to the peptides can be used in immunoassays to detect or
 CC quantify NANBV antigens in liver tissue and blood. Preferred poly-
 CC peptides include residues 1-30, -115, or 2012; 47-77; 116-191;
 CC 132-207 or 298; 230-238 or -263; 287-300; 293-330; 390-729; 730-
 CC 1005; 1006-1614; 1384-1414; 1615-1862; 1737-1767; 1863-2012; and
 CC 2013-3010.
 CC The sequence is also disclosed in EP-464287 (SEQ ID NO 1).
 CC See R20091 for details of this specification.
 SQ Sequence 3010 AA;

Query Match 100.0%; Score 4516; DB 4; Length 3010;
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;
 Matches 631; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1027 apitaysgqtrgllgclitsltgrdknqgevegyvstatqsfllatcvcwcyvhyag 1086
 |||||||
 QY 1 APTAYSQOTRGILGCLITSLGRDKNOVEGEVYSTATQSFLLATCVNGCWYVHGAG 60
 |||||||

Db 1087 sktlaapkgpiltqmytnvqdlvgwpxkpgarsltprctgssdlyvttrhadviprrrg 1146
 |||||||
 QY 61 SKTLAAPKGPITQMTNTNDQLVGMPKPGARSLPCTCGSSDLYVTTRHADVIPRRRG 120
 |||||||

Db 1147 dsrgslspprvsylyksgsggpllpfghnvgifraavcttgvakavdlyvvesmetmr 1206
 |||||||
 QY 121 DSRGSLSPRPVSYLYKSGSGGPLCPFGHNAVGFRAAVCTRGVAAVDFVPVSMETMR 180
 |||||||

Db 1207 spvftdnssppavpqsfgyahlhaprgsgsktkvpaayaagykxlvlnpsvaatlqfga 1266
 |||||||
 QY 181 SPVFTDNSSPPAVPQSGVYAHNHAPRGSGSKTKVPAAYAAGYKXVLVNPVAATLGFGA 240
 |||||||

Db 1267 ymskagidpnrltgyvtlttgavrvtystkykfladggsggagdydliddechstdsttl 1326
 |||||||
 QY 241 YMSKAGIDPNRLTGYVTLTGAARYTYSYKFKFLADGGSGGAGDYDIIIDECHSTDSTTI 300
 |||||||

Db 1327 lqigtvldgaetagarlyvlatatppgstvtrphnleeralntgeiprvygaileair 1386
 |||||||
 QY 301 LGIGTVLDGAETAGARLYVLATATPPGSTVTRPHNLEERALTNGEILPRTYGAILEAIR 360
 |||||||

Db 1387 ggrhllfchskkkckdelaaeklgslqinaavayrygldsvilptlgdvvvaatqalntgyts 1446
 |||||||
 QY 361 GGRHLLFCHSKKKCKDELAALKSLGLGINAAVYRGLDVSVIPIGDDVVVAATQALMNGYTS 420
 |||||||

Db 1447 dfdsyldcntcvtqtvdfslldptfletttvpqavsisqrrgrtgrgrylrvtpge 1506
 |||||||
 QY 421 DFDYLDNCVTQVTEVDFSLDPTFTTETTTVPQDAVSRSQRGRTRGRGRYRTPGE 480
 |||||||

Db 1507 rpsgmfdssvllcecydagagavreltpaetsvrlravlnltpglpvsgdhlefesvftgl 1566
 |||||||
 QY 481 RPSGMFDSSVLLCECYDAGAGAVELTPAETSVRLRAVLNPLGPVODHLEFMSVFTGLT 540
 |||||||

Db 1567 hldahflsgtkagdaafpylvaaycatvcaragaqppswdgmwkcilrlkptlhpripily 1626
 |||||||
 QY 541 HLD AHLSGTKAGDAAFPYLVAAYCATVCARAGAPPSWDMWKCILRLKPTLHGRIPILY 600
 |||||||

Db 1627 rlgavgnevrlthptlckymacsadlevvt 1657
 |||||||
 QY 601 RLGAQVNEVRLTHPTIKYIMACMSADLEVT 631
 |||||||

Key Location/Qualifiers
 FT Protein 1..115
 FT /label= C
 FT /note= "core protein"
 FT Protein 116..191
 FT /label= M
 FT /note= "matrix protein"
 FT Protein 192..389
 FT /label= E
 FT /note= "envelope protein"
 FT Protein 390..729
 FT /label= NS1
 FT Protein 730..1006
 FT /label= NS2
 FT Protein 1007..1614
 FT /label= NS3
 FT Protein 1615..1862
 FT /label= NS4
 FT Protein 1863..2012
 FT /label= NS4b
 FT Protein 2013..3010

FT Protein
 FT /label= NS5
 FT EP-464287-A.
 PD 08-JAN-1992.
 PE 28-DEC-1990; 314371.
 PR 25-JUN-1990; JP-167466.
 PR 31-AUG-1990; JP-230921.
 PR 09-NOV-1990; JP-305603.
 PI (OSAU) Osaka University.
 PI Okayama H, Fuke I, Morl C, Takamizawa A, Yoshida I.
 DR WPI: 92-009617/02.
 DR N-PSDB: 021829.
 PT Non-A, non-B hepatitis virus (NANBV) particles - as vaccine, immuno-
 PT diagnostics and screening agents for NANBV, and to remove NANBV from
 PT blood.
 PS Claim 3; Fig 2; 89pp; English.
 CC The sequence was deduced from several overlapping "BK" cDNA clones
 CC obtd. by "gene walking" using a cDNA clone isolated from a library
 CC prepd. from NANBV RNA. Antigenic polypeptides from the sequence
 CC can be used as immunogens for vaccine prodn. Antibodies raised to the
 CC and as immunogens for vaccine prodn. Antibodies raised to the
 CC peptides can be used in immunoassays to detect or quantify NANBV
 CC antigens in liver tissue and blood. Preferred polypeptides are
 CC include residues 1-30, -115, or 2012; 47-77; 116-191; 192-207 or
 CC -298; 230-238 or -263; 293-300; 293-330; 390-729; 730-1005; 1006-
 CC 1614; 1384-1414; 1615-1862; 1737-1767; 1863-2012; and 2013-3010.
 CC The sequence is also disclosed in EP-463848 (SEQ ID NO 1) in
 CC which a virus particle contg. antigens encoded by the sequence is
 CC claimed. See R20111 for details of this specification.
 SQ Sequence 3010 AA;

Query Match 100.0%; Score 4516; DB 4; Length 3010;
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;
 Matches 631; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1027 apitaysgqtrgllgclitsltgrdknqgevegyvstatqsfllatcvcwcyvhyag 1086
 |||||||
 QY 1 APTAYSQOTRGILGCLITSLGRDKNOVEGEVYSTATQSFLLATCVNGCWYVHGAG 60
 |||||||

Db 1087 sktlaapkgpiltqmytnvqdlvgwpxkpgarsltprctgssdlyvttrhadviprrrg 1146
 |||||||
 QY 61 SKTLAAPKGPITQMTNTNDQLVGMPKPGARSLPCTCGSSDLYVTTRHADVIPRRRG 120
 |||||||

Db 1147 dsrgslspprvsylyksgsggpllpfghnvgifraavcttgvakavdlyvvesmetmr 1206
 |||||||
 QY 121 DSRGSLSPRPVSYLYKSGSGGPLCPFGHNAVGFRAAVCTRGVAAVDFVPVSMETMR 180
 |||||||

Db 1207 spvftdnssppavpqsfgyahlhaprgsgsktkvpaayaagykxlvlnpsvaatlqfga 1266
 |||||||
 QY 181 SPVFTDNSSPPAVPQSGVYAHNHAPRGSGSKTKVPAAYAAGYKXVLVNPVAATLGFGA 240
 |||||||

Db 1267 ymskagidpnrltgyvtlttgavrvtystkykfladggsggagdydliddechstdsttl 1326
 |||||||


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QY 241 YMSKAGIDPNIRIGVRRITTCGAPVTSYNGKFLADGGSGGAGNDIICDECHSTDSITI 300
Db 1327 Iqfvtvldgaetagarlvvatatppgsvtvphnpiievaalsnteliefygaipiair 1386
QY 301 LGIGTVLDOAETAGARLVVATATPPGSVTVPHNPIIEVALSNTGEIPFYGAIPIDAIR 360
Db 1387 ggrhlifchskkkcdelaaklsqjinaavayrgldvsvipicigdvvvvacaalmtgytg 1446
QY 361 GGRHLIFCHSKKKCDELAAKLSGJINAVAYRGLDVSVIPTIGDVVVVATDALMTGYTG 420
Db 1447 dfgsvldcncvtqvtvdfslaprtfietttvpgdavsrsgrgrtgrgriglyfvtpge 1506
QY 421 DFDSDVDCNCTVQTQVDFSLDPTFTTETTPQDAVSRSQGRGRGRGRGRGRGRGRGR 480
Db 1507 rpsgmfdssvlylcecydagcaweltpaetsvrlaylnthpqlpyvcdhllefesvftgt 1566
QY 481 RPSGMFDSVLYLCECYDAGCAWELTPAETSVRLRAYLNTGQLPYVCDHLEFESVFTGLT 540
Db 1567 hidahfistqkqagdnfpylvaygatvcaragappswdgmwkcldlrkptlhnpptlly 1626
QY 541 HIDAHFISQTQKQADNFPYLVAYGATVCAARAQAPPSWDGMWKCILRLKPTLHNPPTL 600
Db 1627 rlgavgnevltlhpikkyimacmsadlevyt 1657
QY 601 RLGAQVNEVTLTHTPTIKYIMACMSADLEVT 631

RESULT 3
ID R82854 standard; protein; 631 AA.
AC R82854;
DT 04-FEB-1996 (first entry)
DE NS3 serine protease domain.
KW NS3: serine protease; hepatitis C virus; HCV; NS4A; therapy.
OS Hepatitis C virus.
FH key Location/Qualifiers
FT Misc.difference 78
FT /note= "represented by Cal in the specification"
FT Misc.difference 132
FT /note= "represented by Cal in the specification"
FT /note= "represented by Lgu"
FT Misc.difference 338
FT /note= "represented in the specification by Lgu"
FT /note= "represented by Lgu"
FT Misc.difference 454
FT /note= "represented in the specification by Aps"
PN W09522985-A1.
PD 31-ANG-1995.
PF 14-FEB-1995; IT0018.
PR 23-FEB-1994; IT-RM0092.
PA (RICE-) IST RICECHE BIOL MOLECOLARE ANGELETTI.
PI De Francesco R, Falla C, Tomei L;
DR WPI: 95-311381/40.
PT In vitro reproduction of hepatitis C virus NS3 protease activity -
PT by including the NS4A cofactor in the mixt., useful for screening
PT cpds. that inhibit NS3
PS Claim 6; Page 16-18; 26pp; English.
CC This sequence represents the Hepatitis C virus (HCV) NS3 serine protease
CC domain. The NS3 serine protease domain requires NS4A (see R82855) as a
CC cofactor. Optimal serine protease activity is obtained when NS4A and NS3
CC are present in a 1:1 ratio. The cleavage site between these two proteins
CC on the HCV genome can be mutated so that the components remain covalently
CC bonded. These sequences are included in a composition that can be used
CC in an assay system. This assay system can be used to select compounds
CC that inhibit NS3 activity, e.g. potential therapeutic agents. NS4A can
CC be used for screening enzyme inhibitors.
SQ Sequence 631 AA;

```

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Query Match 99.4%; Score 4490; DB 15; Length 631;
Best Local Similarity 99.4%; Pred No. 0.00e+00;
Matches 627; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 1 apitvsgatvrljalciltslvgdkngvgegyvvtatqslfctcvvgywtyhag 60
QY 1 APTIVSQAOTRLILGLIITSLTGRKNGVEGVSIVVSTATQSLFCTCVVGYWTYHAG 60

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Db 61 sktlaapkpiltgmytnxdgdlvwpkxppgarrsttpctcgssdlylvtrhadvpyrrrg 120
QY 61 SKTLAAPKPIITGMATINWDQDLVGMKPPGARRSLPCTCGSSDLYLVTRHADVPIYRRRG 120
Db 121 dsrsgllspprpxsylvkssgspgllcpfghavgyfiraactvgaakavfyvesmetmr 180
QY 121 DSRGSLLSPPRPXSYLVKSSGSPGLLCPFGHAVGYFIRAAC TVGAAKAVFYVESMETMR 180
Db 181 spvftdnssppavpqsfgvahhaptsgskctkypaaaggykvlylupsvaatlfgga 240
QY 181 SPVFTDNSSPPAVPQSFQVAHLHAPTSGSKSTKYPAAVAAQGYKVLYLNPVSAATLFGGA 240
Db 241 ymskagidpnirigvrrittcgavtstykgfladggsggagndiicdechstdsti 300
QY 241 YMSKAGIDPNIRIGVRRITTCGAPVTSYNGKFLADGGSGGAGNDIICDECHSTDSTI 300
Db 301 lqfvtvldgaetagarlvvatatppgsvtvphnpiievaalsnteliefygaipiair 360
QY 301 LGIGTVLDOAETAGARLVVATATPPGSVTVPHNPIIEVALSNTGEIPFYGAIPIDAIR 360
Db 361 ggrhlifchskkkcdelaaklsqjinaavayrgldvsvipicigdvvvvacaalmtgytg 420
QY 361 GGRHLIFCHSKKKCDELAAKLSGJINAVAYRGLDVSVIPTIGDVVVVATDALMTGYTG 420
Db 421 dfgsvldcncvtqvtvdfslaprtfietttvpgdavsrsgrgrtgrgriglyfvtpge 480
QY 421 DFDSDVDCNCTVQTQVDFSLDPTFTTETTPQDAVSRSQGRGRGRGRGRGRGRGRGR 480
Db 481 rpsgmfdssvlylcecydagcaweltpaetsvrlaylnthpqlpyvcdhllefesvftgt 540
QY 481 RPSGMFDSVLYLCECYDAGCAWELTPAETSVRLRAYLNTGQLPYVCDHLEFESVFTGLT 540
Db 541 hidahfistqkqagdnfpylvaygatvcaragappswdgmwkcldlrkptlhnpptlly 600
QY 541 HIDAHFISQTQKQADNFPYLVAYGATVCAARAQAPPSWDGMWKCILRLKPTLHNPPTL 600
Db 601 rlgavgnevltlhpikkyimacmsadlevyt 631
QY 601 RLGAQVNEVTLTHTPTIKYIMACMSADLEVT 631

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RESULT 4
ID R41435 standard; protein; 2354 AA.
AC R41435;
DT 24-FEB-1994 (first entry)
DE PT-NANBH virus non-structural proteins.
KW Parenterally transmitted non A non B hepatitis; PT-NANBH; NS4;
KW hepatitis C virus; HCV; detection; diagnosis; antigen; vaccine;
KW amplification; primer; polymerase chain reaction; PCR.
OS Parenterally transmitted non A non B hepatitis virus.
PN W09317110-A.
PD 02-SEP-1993.
PF 19-FEB-1993; G00345.
PR 21-FEB-1992; GB-003803.
PA (WELI ) WELICOME FOUND LTD.
PI Parker D, Rodgers BC;
DR WPI: 93-288415/36.
PT N-PDB: Q46195.
PT New recombinant polypeptide for diagnosing hepatitis C - contains
PT three distinct antigens from different viral regions, also useful
PT in protective vaccines
PS Example 1; Page 43-53; 99pp; English.
CC The NS4 region from the 3' region of the PT-NANBH genome (Q46195)
CC is amplified by PCR using primers D224 and D226 (Q46196-97) and
CC the fragment (Q46198) is cloned into a vector and expressed in
CC infected insect cells. The recombinant virus (BHC-19) was able
CC to express the NS4 specific recombinant protein at low levels in
CC the infected insect cells.
CC If at least three different PT-NANBH antigens are used to screen
CC for PT-NANBH, the screening is much more sensitive as compared to
CC the use of only two PT-NANBH antigens. Pref. antigens are
CC described in Q46192-94. Two new antigenic regions of the
CC PT-NANBH genome are given in Q46198-99. Q46202 describes

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CC an improved PT-NANBH recombinant polypeptide.
 SQ Sequence 2354 AA;
 Query Match 97.6%; Score 4407; DB 8; Length 2354;
 Best Local Similarity 96.4%; Pred. No. 0.00e+00;
 Matches 608; Conservative 18; Mismatches 5; Indels 0; Gaps 0;

Db 211 apitarsgtrgllgcltstlgrdkngvegeyqvstataqsfllatcvgwctyhyag 270
 |||
 1 APITARSQOTRGLGCIITSLGRDNQYEGEVYSTAQSLACVAGCWYVHGAG 60
 |||
 Db 271 sktlagpkpplgmytnvqdlyvgwppagarslprctcgssdlylvtlhadviprrrg 330
 |||
 61 SKTLAPKGPPIQMTYNNVODLYGWPKPFGARSLPCTCGSSDLYLVTNHADVIPRRRG 120
 |||
 Db 331 dngslsprpsylkgssgspllcpshavgfiraavctrvakavdfevpsmettr 390
 |||
 121 DNRGSLSPRPVSYLKGSSGSPLLCPGSHAVGIFRAAVCTRGYAKAVDVPVPSMETTR 160
 |||
 Db 391 spvftcnsppavpqsfigyahlhaptsgkstrvpaayaagkykvlvlpvvaatlfiga 450
 |||
 181 SPVFTNNSPPAVPQSFQYAHLMHAPTSGSKSTKVPAAVAAQGYKVLVLPVVAATLGFGA 240
 |||
 Db 451 ymskabgvpnlsgrvrlttgapiytsygkfladgcsgeyadlmdectststl 510
 |||
 241 YMSKAGIDPNITGVRITTTGAPVITYSGKFLADGCSGGAVIDIIDECHSTSTT 300
 |||
 Db 511 lsgltvldgaetagarlvlatatppgsvtvphnlevalnstgeipfygkaipietlk 570
 |||
 301 LGIGTVLDQETRGARLVLATATPPGSVTVPHNLEVALNSTGELPFYGKALPIEALR 360
 |||
 Db 571 gsrhlifchskkkcdelaaklsglgnavaayrgldvsvipdsqdvvvatdmltgytg 630
 |||
 361 GSRHLIFCHSKKKCDELAALSGGINAVAYRGLDVSVIPTIGDVVVAATDMLMGTYTG 420
 |||
 Db 631 dfgsvldcntcvtqtvdffsldpftfletctvpgdavsrsgrtgrtgyrglyrfvppge 690
 |||
 421 DFGSVLDNCNTCVTQIVDFSLDPFTFLETCTVPGDAVSRSQRGTGGRGIVRFVPPGE 460
 |||
 Db 691 rpsgmfsprlcecydagacaweltpaetsvrlraylntgllpvcqdhlfwesvftglt 750
 |||
 481 RPSGMFDSVILCECYDAGCAWELTPRETISVRLRAYLNTGILPVCQDHLFWESVFTGLT 540
 |||
 Db 751 hvdahflsqtkgaqndfpylvaygatvcaragppswdmmwkcilrlkptllgprpilly 810
 |||
 541 HIDAHFLSQTKQAGNDPNYLVAYGATVCARAQAAPPSPMDMMKCLIRLKPILLGPRPILLY 600
 |||
 Db 811 rlgaavnevtlthpikffimacmsadlevvt 841
 |||
 601 RLGAVQNEVTLTHPITIKYIMACMSADLEVVT 631
 |||

RESULT 5
 ID R54099 standard; Protein; 3014 AA.
 AC R54099;
 DT 09-FEB-1995 (first entry)
 DE NANBH E1/E2 protein.
 KM E1/E2 protein; non-A, non-B hepatitis virus; NANBH; signal peptide;
 KW heterogenic; virus; transformation; insect cell; antigen; anti-NANBH;
 KM antibody; hepatitis C virus; HCV; vaccine.
 OS Non-A, non-B hepatitis virus.
 FH Key Location/Qualifiers
 FT Peptide 832..847
 FT /note= "peptide fragment not given in the specification,
 FT but encoded by the given cDNA sequence"
 FT Peptide 1296..1311
 FT /note= "peptide fragment not given in the specification,
 FT but encoded by the given cDNA sequence"
 FT Peptide 1760..1775
 FT /note= "peptide fragment not given in the specification,
 FT but encoded by the given cDNA sequence"
 FT Peptide 2688..2703
 FT /note= "peptide fragment not given in the specification,"

FT but encoded by the given cDNA sequence"
 FN J06141873-A.
 PD 24-MAY-1994.
 PF 13-MAR-1992; 089371.
 PR 13-MAR-1992; JP-089371.
 PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 DR WPI 94-205030/25.
 DR N-PSDB; Q64175.
 PR Virus vector contg hepatitis C virus and signal sequence - useful
 PR in vaccines and in immunological detection
 PS Disclosure; Page 7-19; 23pp; Japanese.
 CC This sequence represents the E1/E2 protein from non-A, non-B hepatitis
 CC virus (NANBH). The cDNA encoding this sequence may be linked to a
 CC signal peptide (754100) from a heterogenic virus so the NANBH
 CC protein may be expressed by a transformed insect cell. This protein
 CC may be used as an antigen in the generation of anti-NANBH antibodies.
 CC These antibodies may be used in a hepatitis C vaccine.
 SQ Sequence 3014 AA;

Query Match 97.5%; Score 4404; DB 10; Length 3014;
 Best Local Similarity 97.0%; Pred. No. 0.00e+00;
 Matches 612; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

Db 1027 apitarsgtrgllgcltstlgrdkngvegeyqvstataqsfllatcvgwctyhyag 1086
 |||
 1 APITARSQOTRGLGCIITSLGRDNQYEGEVYSTAQSLACVAGCWYVHGAG 60
 |||
 Db 1087 sktlagpkpplgmytnvqdlyvgwppagarslprctcgssdlylvtlhadviprrrg 1146
 |||
 61 SKTLAPKGPPIQMTYNNVODLYGWPKPFGARSLPCTCGSSDLYLVTNHADVIPRRRG 120
 |||
 Db 1147 dngslsprpsylkgssgspllcpshavgfiraavctrvakavdfevpsmettr 1206
 |||
 121 DNRGSLSPRPVSYLKGSSGSPLLCPGSHAVGIFRAAVCTRGYAKAVDVPVPSMETTR 180
 |||
 Db 1207 spvftcnsppavpqsfigyahlhaptsgkstrvpaayaagkykvlvlpvvaatlfiga 1266
 |||
 181 SPVFTNNSPPAVPQSFQYAHLMHAPTSGSKSTKVPAAVAAQGYKVLVLPVVAATLGFGA 240
 |||
 Db 1267 ymskabgvpnlsgrvrlttgapiytsygkfladgcsgeyadlmdectststl 1326
 |||
 241 YMSKAGIDPNITGVRITTTGAPVITYSGKFLADGCSGGAVIDIIDECHSTSTT 300
 |||
 Db 1327 lsgltvldgaetagarlvlatatppgsvtvphnlevalnstgeipfygkaipietlk 1386
 |||
 301 LGIGTVLDQETRGARLVLATATPPGSVTVPHNLEVALNSTGELPFYGKALPIEALR 360
 |||
 Db 1387 gsrhlifchskkkcdelaaklsglgnavaayrgldvsvipdsqdvvvatdmltgytg 1446
 |||
 361 GSRHLIFCHSKKKCDELAALSGGINAVAYRGLDVSVIPTIGDVVVAATDMLMGTYTG 420
 |||
 Db 1447 dfgsvldcntcvtqtvdffsldpftfletctvpgdavsrsgrtgrtgyrglyrfvppge 1506
 |||
 421 DFGSVLDNCNTCVTQIVDFSLDPFTFLETCTVPGDAVSRSQRGTGGRGIVRFVPPGE 460
 |||
 Db 1507 rpsgmfsprlcecydagacaweltpaetsvrlraylntgllpvcqdhlfwesvftglt 1566
 |||
 481 RPSGMFDSVILCECYDAGCAWELTPRETISVRLRAYLNTGILPVCQDHLFWESVFTGLT 540
 |||
 Db 1567 hvdahflsqtkgaqndfpylvaygatvcaragppswdmmwkcilrlkptllgprpilly 1626
 |||
 541 HIDAHFLSQTKQAGNDPNYLVAYGATVCARAQAAPPSPMDMMKCLIRLKPILLGPRPILLY 600
 |||
 Db 1627 rlgaavnevtlthpikffimacmsadlevvt 1657
 |||
 601 RLGAVQNEVTLTHPITIKYIMACMSADLEVVT 631
 |||

RESULT 6
 ID R35207 standard; Protein; 3014 AA.
 AC R35207;
 DT 29-JUL-1993 (first entry)
 DE Hepatitis C virus protein.

KW HCV; detection; antigen; vaccine; recombinant.
 OS Hepatitis C virus.
 PN J05068563-A.
 PD 23-MAR-1993.
 PF 17-JUL-1991; 203884.
 PR (KAGAKU) KAGAKU OYOBI KESSEI RYOHO.
 PA WPI: 93-130639/16.
 DR N-PSDB: Q38959.
 PT Nucleotide sequence encoding hepatitis C virus polypeptide - is
 PT useful for detecting HCV infection, esp. in Japan, and as vaccine
 PT against HCV
 PS Claim 2; Page 6-17; 17pp; Japanese.
 CC RNA was extracted from the plasma of Japanese patients whose Hbs
 CC antigen was negative and with a GPT over 100. cDNA was synthesised
 CC from the RNA and cloned into lambda g11 and screened using HCV
 CC infected chimpanzee plasma to isolate HCV clones. The DNA sequence
 CC is useful in detection of HCV virus. The polypeptide it produces
 CC may be used as an antigen in the prepn. of HCV vaccine.
 SQ Sequence 3014 AA;

Query Match 97.4%; Score 4397; DB 7; Length 3014;
 Best Local Similarity 96.7%; Pred. No. 0.00e+00;

Matches 610; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

Db 1027 apitaysgtgrllgclitsltgrkngdgvgeyvtstgtsfllatcngvcwtvyyhag 1086
 QY 1 APTAYSGOTRRLGCIITSLTGROKNOYEGHVQVSTATQSFLLATCNGVCWTVYHAG 60
 Db 1087 sntlsgpkpilaqmytunvqdlvgwppaparsltpctcgssdlylvrthadvpyrrrg 1146
 QY 61 SKTLAPKGPITQMTNVDQLVGMPKPPGARSILPCTCGSSDLTVLRHADVPIYRRRG 120
 Db 1147 dargslspprvpylkgssgppllcpsghavvifraavctrvakavdlyvresmetmr 1206
 QY 121 DSRGSLSPRPVSYLKGSSGGLPCFGHAGVIFRAAVCTRGVAKAVDFVRESMETMR 180
 Db 1207 spvftdssppavpqtfgvahlhaptgsgsktrrypaayatgkykylvlnpsvaatlgyga 1266
 QY 181 SPVFTDNSSPPAVPQSFVYAHHAFTGSGSKTRYPAAAYAAQGYKVLVNPVVAATLGGGA 240
 Db 1267 ymskshgtdpmlrtgvtlittgaptltyctygflladggcsagaydliicdehstddtli 1326
 QY 241 YMSKAHGIDPNIRCTGVRITTTGAPVTYSTYGFLLADGGCSGAYDIIICDECHSTDDTII 300
 Db 1327 lgiqvtlidaetaagarlvvlatatppsgvtpvphnieevalsntgelpfygaipieaim 1386
 QY 301 LGIGTVLDQATAGARLVVLTATPPGSVTPVPHNIEEVALSNTGEIPFYGAIPIEAIR 360
 Db 1387 gvrhllfchskkkcdelaaklsgldlnavayrglsvipstsgdvvvvatdalmtygtg 1446
 QY 361 GGRHLIFCHSKKKCDELAAKLSGLINAVAYRGIDVSVIPITGIVVVAADALMTGYTG 420
 Db 1447 dfgsvidentcvtqtdvdsldptfietltvpgdavsrsgrtrgrtgrtgrtgrtgrtgrt 1506
 QY 421 DFDSDVDCNCTVQTVDFSLDPTFTIETTTVPQDAVSRSQGRGRGRGRGRGRGRGRGRGR 480
 Db 1507 rpsgmfgsvpvlcecydagcayveltpaetsvrlraylntpglpycgdhllefesvftglt 1566
 QY 481 RPSGMFSSVVLCECYDAGCAYVELTPAETSVRLRAYLNTPELPQODHLEWESVFTGLT 540
 Db 1567 hidahflsqtqgaadnfylyaygatvcaragapppsdgmwkcldlkrptlhpptlly 1626
 QY 541 HIDAHPFSQTQAGDNPFIYLYAYGATVCARAQAPPSWDMMKCLIRLKRPTLHGPTPLLY 600
 Db 1627 rlgavnevlthpiltkyimacmsadlevvt 1657
 QY 601 RLGAQNEVTLTHPTITKYIMACMSADLEVT 631

RESULT 7
 ID R82693 standard; Protein; 916 AA.
 AC R82693;

DT 11-NOV-1996 (first entry)
 DE HCV partial proteinase.
 KW proteinase; hepatitis C virus; screening; inhibitor; proteolytic;
 KW identification; cleavage.
 OS Hepatitis C virus.
 PN U07184648-A.
 PD 25-JUL-1995.
 PE 05-FEB-1993; 018854.
 PR 07-FEB-1993; JP-022657.
 PR 18-SEP-1992; JP-249240.
 PR 04-DEC-1992; JP-325303.
 PA (KAEN/) KAENNO K.
 PA (SOYA-) SOYAKU GIUTSU KENKYUSHO KK.
 PA (SUMO) SUMITOMO METAL IND LTD.
 DR WPI: 95-287962/38.
 DR N-PSDB: T03959.
 PT An HCV proteinase active substance - which has activity as an
 PT anti-HCV agent and can be used to screen for proteinase inhibitors
 PS Claim 3; Page 24-27; 52pp; Japanese.
 CC The present sequence is that of a partial proteinase isolated from
 CC Hepatitis C virus (HCV). The proteinase can be used as an anti-HCV
 CC agent. It can also be used to screen cpts. for their ability to
 CC inhibit its proteolytic activity. In this way proteinase inhibitors
 CC can be identified.
 SQ Sequence 916 AA;

Query Match 97.2%; Score 4389; DB 18; Length 916;
 Best Local Similarity 95.7%; Pred. No. 0.00e+00;

Matches 604; Conservative 21; Mismatches 6; Indels 0; Gaps 0;

Db 36 apitaysgtgrllgclitsltgrkngdgvgeyvtstgtsfllatcngvcwtvyyhag 95
 QY 1 APTAYSGOTRRLGCIITSLTGROKNOYEGHVQVSTATQSFLLATCNGVCWTVYHAG 60
 Db 96 sktlaqpkpiltqmytunvqdlvgwppaparsltpctcgssdlylvrthadvpyrrrg 155
 QY 61 SKTLAPKGPITQMTNVDQLVGMPKPPGARSILPCTCGSSDLTVLRHADVPIYRRRG 120
 Db 156 dargslspprvpylkgssgppllcpsghavvifraavctrvakavdlyvresmetmr 215
 QY 61 SKTLAPKGPITQMTNVDQLVGMPKPPGARSILPCTCGSSDLTVLRHADVPIYRRRG 120
 Db 121 DSRGSLSPRPVSYLKGSSGGLPCFGHAGVIFRAAVCTRGVAKAVDFVRESMETMR 180
 QY 121 DSRGSLSPRPVSYLKGSSGGLPCFGHAGVIFRAAVCTRGVAKAVDFVRESMETMR 180
 Db 216 spvftdssppavpqtfgvahlhaptgsgsktrrypaayatgkykylvlnpsvaatlgyga 275
 QY 181 SPVFTDNSSPPAVPQSFVYAHHAFTGSGSKTRYPAAAYAAQGYKVLVNPVVAATLGGGA 240
 Db 276 ymskshgtdpmlrtgvtlittgaptltyctygflladggcsagaydliicdehstddtli 335
 QY 276 YMSKAHGIDPNIRCTGVRITTTGAPVTYSTYGFLLADGGCSGAYDIIICDECHSTDDTII 300
 QY 241 YMSKAHGIDPNIRCTGVRITTTGAPVTYSTYGFLLADGGCSGAYDIIICDECHSTDDTII 300
 Db 336 lgiqvtlidaetaagarlvvlatatppsgvtpvphnieevalsntgelpfygaipieaim 395
 QY 301 LGIGTVLDQATAGARLVVLTATPPGSVTPVPHNIEEVALSNTGEIPFYGAIPIEAIR 360
 Db 396 gvrhllfchskkkcdelaaklsgldlnavayrglsvipstsgdvvvvatdalmtygtg 455
 QY 361 GGRHLIFCHSKKKCDELAAKLSGLINAVAYRGIDVSVIPITGIVVVAADALMTGYTG 420
 Db 456 dfgsvidentcvtqtdvdsldptfietltvpgdavsrsgrtrgrtgrtgrtgrtgrtgrt 515
 QY 421 DFDSDVDCNCTVQTVDFSLDPTFTIETTTVPQDAVSRSQGRGRGRGRGRGRGRGRGRGR 480
 Db 516 rpsgmfgsvpvlcecydagcayveltpaetsvrlraylntpglpycgdhllefesvftglt 575
 QY 481 RPSGMFSSVVLCECYDAGCAYVELTPAETSVRLRAYLNTPELPQODHLEWESVFTGLT 540
 Db 576 hidahflsqtqgaadnfylyaygatvcaragapppsdgmwkcldlkrptlhpptlly 635
 QY 541 HIDAHPFSQTQAGDNPFIYLYAYGATVCARAQAPPSWDMMKCLIRLKRPTLHGPTPLLY 600
 Db 636 rlgavnevlthpiltkyimacmsadlevvt 666
 QY 601 RLGAQNEVTLTHPTITKYIMACMSADLEVT 631

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RESULT 8
ID R82694 standard: Protein: 3010 AA.
AC R82694;
DT 14-NOV-1996 (first entry)
DE Partial HCV non-structural polypeptide.
KW proteinase; hepatitis C virus; screening; inhibitor; proteolytic;
OS identification; cleavage.
HE Hepatitis C Virus.
FH Key Location/Qualifiers
FT Protein 898..1233
FT /note= "partial proteinase; see R82692"
FT Protein 992..1907
FT /note= "partial proteinase; see R82693"
PN J07184648-A.
PD 25-JUL-1995.
PE 05-FEB-1993; 018854.
PR 07-FEB-1992; JP-022657.
PR 18-SEP-1992; JP-249240.
PR 04-DEC-1992; JP-325303.
PA (KAEN/K.) KAENNO K.
PA (SOYA-) SOYAKU GIJUTSU KENKYUSHO KK.
PA (SOMO-) SOMITOMO METAL IND LTD.
DR WPI; 95-287962/38.
DR N-PSDB; T03960.
PT An HCV proteinase active substance - which has activity as an
PT anti-HCV agent and can be used to screen for proteinase inhibitors
PS Disclosure; Page 39-48; 52pp; Japanese.
CC The present sequence is a partial Hepatitis C Virus (HCV) polypeptide
CC from the non-structural region. Partial proteinase sequences (R82692-
CC 93) are contained within this sequence. The proteinases can be used as
CC anti-HCV agents. They can also be used to screen cDNAs for their ability
CC to inhibit their proteolytic activity. In this way proteinase inhibitors
CC can be identified.
SQ Sequence 3010 AA;
Query Match 97.2%; Score 4389; DB 18; Length 3010;
Best Local Similarity 96.0%; Pred. No. 0.00e+00;
Matches 606; Conservative 19; Mismatches 6; Indels 0; Gaps 0;
Db 1027 apitaysgqtrllgclltslgrdkngydgvyrlststqsfllatcngvwttyhag 1086
QY 1 apitaysgqtrllgclltslgrdkngydgvyrlststqsfllatcngvwttyhag 60
Db 1087 skllagpkpklqmylvnvgdglvwppapgsamrptcgssdlylvtrhadvyprrrg 1146
QY 1 skllagpkpklqmylvnvgdglvwppapgsamrptcgssdlylvtrhadvyprrrg 60
Db 1147 jargslisprlsylyksgsgpplcpssglnvgifraavctryvakavdflpvesmetmr 1206
QY 1 jargslisprlsylyksgsgpplcpssglnvgifraavctryvakavdflpvesmetmr 180
Db 1207 spvfdnssppavpqtfgvahlhaprgskstkypaayaggykylvlnpsaatlfgfa 1266
QY 1 spvfdnssppavpqtfgvahlhaprgskstkypaayaggykylvlnpsaatlfgfa 240
Db 1267 ymskahglsenartgrrtlttgsplystycckflaaggsgsgaydliidechstdstli 1326
QY 1 ymskahglsenartgrrtlttgsplystycckflaaggsgsgaydliidechstdstli 300
Db 1327 lslgtvldgaetagarlvlatatppgsiltvphnievalnstgeipfykaipieaik 1386
QY 1 lslgtvldgaetagarlvlatatppgsiltvphnievalnstgeipfykaipieaik 360
Db 1387 gghhlfchskkkcdelaaklglgljnavayryglavsvlpsgdvrvvatdalmrgftg 1446
QY 1 gghhlfchskkkcdelaaklglgljnavayryglavsvlpsgdvrvvatdalmrgftg 420
Db 1447 dfaavldcncvctvdtsldpftlettlpddavsrqzgrtgrsglyrfttpe 1506
QY 1 dfaavldcncvctvdtsldpftlettlpddavsrqzgrtgrsglyrfttpe 480

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Db 1507 rpsgmfdssvllcecydagawelyetpsetvrlraylntgplvpcqdhlefesvftgl 1566
QY 481 rpsgmfdssvllcecydagawelyetpsetvrlraylntgplvpcqdhlefesvftgl 540
Db 1567 hiaahfistckkgaadnlpvlyavgatvcaragappswdgmwkcillrlkplthgptlly 1626
QY 541 hiaahfistckkgaadnlpvlyavgatvcaragappswdgmwkcillrlkplthgptlly 600
Db 1627 rlgaqnevtlthpirtkymacmsadleevt 1657
QY 601 rlgaqnevtlthpirtkymacmsadleevt 631
RESULT 9
ID R68864 standard: Protein: 3010 AA.
AC R68864;
DT 06-DEC-1995 (first entry)
DE Hepatitis C virus RNA helicase.
KW Hepatitis C virus; HCV; non-A non-B; helicase gene; RNA helicase;
KW baculovirus; recombinant production.
OS Hepatitis C virus.
FH Key Location/Qualifiers
FT Region 196..198
FT /label= N-linked glycosylation site
FT Region 209..211
FT /label= N-linked glycosylation site
FT Region 234..236
FT /label= N-linked glycosylation site
FT Region 250..252
FT /label= N-linked glycosylation site
FT Region 305..307
FT /label= N-linked glycosylation site
FT Region 325..327
FT /label= N-linked glycosylation site
FT Region 417..419
FT /label= N-linked glycosylation site
FT Region 423..425
FT /label= N-linked glycosylation site
FT Region 430..432
FT /label= N-linked glycosylation site
FT Region 448..450
FT /label= N-linked glycosylation site
FT Region 532..534
FT /label= N-linked glycosylation site
FT Region 536..538
FT /label= N-linked glycosylation site
FT Region 576..578
FT /label= N-linked glycosylation site
FT Region 623..625
FT /label= N-linked glycosylation site
FT Region 645..647
FT /label= N-linked glycosylation site
FT Region 1213..1215
FT /label= N-linked glycosylation site
FT Region 1255..1257
FT /label= N-linked glycosylation site
FT Region 2041..2043
FT /label= N-linked glycosylation site
FT Region 2077..2079
FT /label= N-linked glycosylation site
FT Region 2240..2242
FT /label= N-linked glycosylation site
FT Region 2788..2790
FT /label= N-linked glycosylation site
PN J06319583-A.
PD 22-NOV-1994.
PE 18-SEP-1992; 249241.
PR 18-SEP-1992; JP-249241.
PA (SOYA-) SOYAKU GIJUTSU KENKYUSHO KK.
PA WPI; 95-040330/06.
DR N-PSDB; Q81559.
PT Expression of hepatitis C virus helicase gene in baculovirus -
PT useful for large scale produ. of RNA helicase.

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PS Claim 1; Fig 1-4; 9pp; Japanese.
 CC 081559 encodes R6864 hepatitis C virus (HCV) RNA helicase. The
 CC DNA was used in the construction of an expression vector, which
 CC was used to transform a baculovirus host. The transformed
 CC baculovirus could then be used for the recombinant prodn. of
 CC HCV RNA helicase.
 SQ Sequence 3010 AA;

Query Match 97.18; Score 4383; DB 14; Length 3010;
 Best Local Similarity 95.9%; Pred. No. 0.00e+00;
 Matches 605; Conservative 20; Mismatches 6; Indels 0; Gaps 0;

Db 1027 apitaysgqtrgllgclitslgrdknqvgdevqlstqsfllacvngcwtvvhgag 1086
 |||||||
 QY 1 APTTASQQRGLGCLITSLTGRDNQVGEVQVSTAQSLACVNGVCMVTYVHGAG 60
 Db 1087 sktlaapkgpiltqmylnvddqdlvgwppaparsmtpctcgssdlylvttrhadvpyrrng 1146
 |||||||
 QY 61 SKTLAAPKGPILTQMTNVDDLVGMPKPRGARSILPTCTGSSDLVYTRHADVTPVRRRG 120
 Db 1147 dsrgslsprpilsylkgssggpdlcpshvvgiffravctryakavdflpvesmetmr 1206
 |||||||
 QY 121 DSRGSLSPRPVSYLKSSGSGPLCPFGHVGIFRAVCTRGVAKAVDPVPSMETMR 180
 Db 1207 spvfdnsppavpvtffgahlhaptgsgsktkvpaayaaggykxvlvlpvsaatlqfga 1266
 |||||||
 QY 181 SEVFDNNSPPAVPVSFOVAHLHAPFGSGSKTKVPAAYAAGGYKXVLVNPVSAATLGFGA 240
 Db 1267 ymskaghiepnulrtgrrlttggpltystycckfladggcgsgaydlldcehststtl 1326
 |||||||
 QY 241 YMSKAGHIDPNRTGVRITTTGAPVYTYGKFLADGGCGSGAYDILIDCEHSTSTTL 300
 Db 1327 lqigevldaeatagarlvvlatatppgsitvphnieevalsntgelbfygaipdeaik 1386
 |||||||
 QY 301 LGIGVLDQAEATAGARLVVLTATPPGSVTPVHPNIEEVALSNTGELPFYGAIPDEAIR 360
 Db 1387 ggrhllfchskkkcdelaakltglnavayrrgldsviprsgdvvvatadalmgtfgy 1446
 |||||||
 QY 361 GGRHLIFCHSKKKCDELAAKLSGLINAVAYRRGLDVSVIPRIGDVVVVATADALMTGYTG 420
 Db 1447 dfdsvidcntcvtqvdfsldptfiettlpqdavsraqrrgrgrgryrrfvtgpe 1506
 |||||||
 QY 421 DFDSVIDCNTCVTQVDFSLDPTFIETTTVPQDAVSRSQRRGRGRGRGRIYRFTVPEE 480
 Db 1507 rpsgmfdssvllcecydaacaweyltpaetsvrlraylntpglpvcqdhlefesvftgt 1566
 |||||||
 QY 481 RPSGMFDSSVLLCECYDAGCAWYELTPAETSVRLRAYLNTPGLPVQDHLFEMESVFTGLT 540
 Db 1567 hidahflsgtkagqdnlylvaqatvcaaraqapppswdgmwkcilrlkptlhgpptilly 1626
 |||||||
 QY 541 HIDAHLFSGTKAQAGDNFYLVAIQATVCAARAQAPPPSWDQMKCLIRLKPILHGPPTILLY 600
 Db 1627 rlgavqnevtlthpiktyimacsadlevvt 1657
 |||||||
 QY 601 RLGAQNQNEVTLTHPIKTYIMACMSADLEVT 631
 RESULT 10
 ID R68622 standard; Protein; 3010 AA.
 AC R68622;
 DT 16-OCT-1995 (first entry)
 DE HCV protein cleavable with new serine proteinase.
 KW proteinase; serine; cleavage; hepatitis C virus; HCV.
 OS Hepatitis C Virus.
 FH Key Location/Qualifiers
 FT Cleavage_site 2419..2420
 FT /note="Serine protease cleavage site"
 PN J06315377-A.
 PD 15-NOV-1994.
 PE 06-MAY-1993; 105666.
 PR 06-MAY-1993; JP-105666.
 RA (KAEN)/ KAENNO K.
 PA (SOYA-) SOYAKU GIJUTSU KENKYUSHO KK.

PA (SUMO) SUMITOMO METAL IND LTD.
 DR WPI: 95-032330/05.
 DR N-PSDB: Q80498.

PT New HCV originated proteinase active substance - used for
 PT site-specific cleavage by an intermolecular reaction and the
 PT purification thereof
 PS Disclosure: Page 10-19; 23pp; Japanese.
 CC This protein from HCV (hepatitis C virus) (encoded by Q80498) is
 CC cleaved between amino acids 2419 and 2420, by a new serine protease,
 CC contg. the sequence of R68621. The proteinase is purified as a fused
 CC product with the dihydrofolate reductase protein by using a methotrexate
 CC column. It can be used for the development of an inhibitor for HCV
 CC proteinase.
 SQ Sequence 3010 AA;

Query Match 96.9%; Score 4377; DB 13; Length 3010;
 Best Local Similarity 95.9%; Pred. No. 0.00e+00;
 Matches 605; Conservative 19; Mismatches 7; Indels 0; Gaps 0;

Db 1027 apitaysgqtrgllgclitslgrdknqvgdevqlstqsfllacvngcwtvvhgag 1086
 |||||||
 QY 1 APTTASQQRGLGCLITSLTGRDNQVGEVQVSTAQSLACVNGVCMVTYVHGAG 60
 Db 1087 sktlaapkgpiltqmylnvddqdlvgwppaparsmtpctcgssdlylvttrhadvpyrrng 1146
 |||||||
 QY 61 SKTLAAPKGPILTQMTNVDDLVGMPKPRGARSILPTCTGSSDLVYTRHADVTPVRRRG 120
 Db 1147 dsrgslsprpilsylkgssggpdlcpshvvgiffravctryakavdflpvesmetmr 1206
 |||||||
 QY 121 DSRGSLSPRPVSYLKSSGSGPLCPFGHVGIFRAVCTRGVAKAVDPVPSMETMR 180
 Db 1207 spvfdnsppavpvtffgahlhaptgsgsktkvpaayaaggykxvlvlpvsaatlqfga 1266
 |||||||
 QY 181 SEVFDNNSPPAVPVSFOVAHLHAPFGSGSKTKVPAAYAAGGYKXVLVNPVSAATLGFGA 240
 Db 1267 ymskaghiepnulrtgrrlttggpltystycckfladggcgsgaydlldcehststtl 1326
 |||||||
 QY 241 YMSKAGHIDPNRTGVRITTTGAPVYTYGKFLADGGCGSGAYDILIDCEHSTSTTL 300
 Db 1327 lqigevldaeatagarlvvlatatppgsitvphnieevalsntgelbfygaipdeaik 1386
 |||||||
 QY 301 LGIGVLDQAEATAGARLVVLTATPPGSVTPVHPNIEEVALSNTGELPFYGAIPDEAIR 360
 Db 1387 ggrhllfchskkkcdelaakltglnavayrrgldsviprsgdvvvatadalmgtfgy 1446
 |||||||
 QY 361 GGRHLIFCHSKKKCDELAAKLSGLINAVAYRRGLDVSVIPRIGDVVVVATADALMTGYTG 420
 Db 1447 dfdsvidcntcvtqvdfsldptfiettlpqdavsraqrrgrgrgryrrfvtgpe 1506
 |||||||
 QY 421 DFDSVIDCNTCVTQVDFSLDPTFIETTTVPQDAVSRSQRRGRGRGRGRIYRFTVPEE 480
 Db 1507 rpsgmfdssvllcecydaacaweyltpaetsvrlraylntpglpvcqdhlefesvftgt 1566
 |||||||
 QY 481 RPSGMFDSSVLLCECYDAGCAWYELTPAETSVRLRAYLNTPGLPVQDHLFEMESVFTGLT 540
 Db 1567 hidahflsgtkagqdnlylvaqatvcaaraqapppswdgmwkcilrlkptlhgpptilly 1626
 |||||||
 QY 541 HIDAHLFSGTKAQAGDNFYLVAIQATVCAARAQAPPPSWDQMKCLIRLKPILHGPPTILLY 600
 Db 1627 rlgavqnevtlthpiktyimacsadlevvt 1657
 |||||||
 QY 601 RLGAQNQNEVTLTHPIKTYIMACMSADLEVT 631
 RESULT 11
 ID R82696 standard; Protein; 923 AA.
 AC R82696;
 DT 14-NOV-1996 (first entry)
 DE HCV partial proteinase.
 KW proteinase; hepatitis C virus; screening; inhibitor; proteolytic;
 KW identification; cleavage.
 OS Hepatitis C Virus.
 PN J07184648-A.

PD 25-JUL-1995.
PE 05-FEB-1993; 018854.
PR 07-FEB-1992; JP-022657.
PR 18-SEP-1992; JP-249240.
PR 04-DEC-1992; JP-325303.
PA (KAEN/) KAENNO K.
PA (SOYA-) SOYAKU GIJUTSU KENKYUSHO KK.
PA (SUMO) SUMITOMO METAL IND LTD.
DR WPI: 95-287962/38.
DR N-PSD3: T03985.
PI An HCV proteinase active substance - which has activity as an
PI anti-HCV agent and can be used to screen for proteinase inhibitors
PS Example 2: Page 33-39; 52pp; Japanese.
CC The present sequence (contg. R82693) is that of a partial proteinase
CC isolated from Hepatitis C Virus (HCV). The proteinase can be used
CC as an anti-HCV agent. It can also be used to screen opds. for their
CC ability to inhibit its proteolytic activity. In this way proteinase
CC inhibitors can be identified.
SQ Sequence 923 AA;

Query Match 96.5%; Score 4360; DB 18; Length 923;

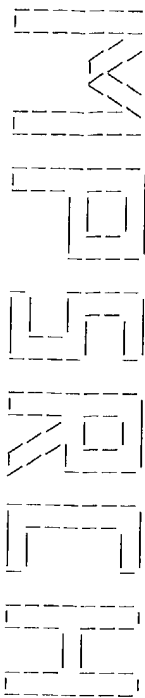
Best Local Similarity 95.2%; Pred. No. 0.00e+00;

Matches 601; Conservative 23; Mismatches 7; Indels 0; Gaps 0;

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QY 1 apitaysgqtglglqclitslgrdkngydgewy]statgsflatcvgvcwtvynag 60
DB 98 sktlagpkpkitqmytnvqgd]vwpappparsmptcgssdlylvtrhadviprrrg 157
QY 61 sktlagpkpkitqmytnvqgd]vwpappparsmptcgssdlylvtrhadviprrrg 120
DB 158 dargsl]sprpyl]ksgsgp]vpcpsghv]ffraavctrvakavd]ipvesmetmr 217
QY 121 dargsl]sprpyl]ksgsgp]vpcpsghv]ffraavctrvakavd]ipvesmetmr 180
DB 218 spv]tdnssppavpqlfgyah]haptgskstkypaayagrykv]vlnpsvaatl]gfga 277
QY 181 spv]tdnssppavpqlfgyah]haptgskstkypaayagrykv]vlnpsvaatl]gfga 240
DB 278 ymskag]iepn]rtgyrt]lttsgp]lcystryck]ladggcgsgayd]i]dechstdstl 337
QY 241 ymskag]iepn]rtgyrt]lttsgp]lcystryck]ladggcgsgayd]i]dechstdstl 300
DB 338]g]q]t]v]ld]ga]e]ta]ga]r]lv]a]ta]tp]ps]i]t]v]p]h]n]e]a]l]s]n]t]g]e]i]p]f]y]k]a]i]p]e]a]k 397
QY 301]g]q]t]v]ld]ga]e]ta]ga]r]lv]a]ta]tp]ps]i]t]v]p]h]n]e]a]l]s]n]t]g]e]i]p]f]y]k]a]i]p]e]a]k 360
DB 398 ggrh]l]f]ch]s]k]k]k]k]d]e]l]a]a]k]t]g]l]n]a]v]a]y]r]g]l]d]v]s]v]t]s]g]d]v]v]v]a]t]d]a]l]m]t]g]f]g 457
QY 361 ggrh]l]f]ch]s]k]k]k]k]d]e]l]a]a]k]t]g]l]n]a]v]a]y]r]g]l]d]v]s]v]t]s]g]d]v]v]v]a]t]d]a]l]m]t]g]f]g 420
DB 458 dfgs]v]d]c]n]t]c]v]t]g]t]d]f]s]i]d]p]t]f]i]e]t]t]l]p]d]a]v]s]r]a]g]r]t]g]r]g]s]l]y]r]f]t]p]g 517
QY 421 dfgs]v]d]c]n]t]c]v]t]g]t]d]f]s]i]d]p]t]f]i]e]t]t]l]p]d]a]v]s]r]a]g]r]t]g]r]g]s]l]y]r]f]t]p]g 480
DB 518 rpsgm]d]s]v]l]c]e]y]d]a]g]a]c]a]w]e]l]t]p]a]e]t]v]r]l]r]a]y]l]n]t]p]g]l]v]c]q]d]h]e]f]w]e]s]v]t]g]t 577
QY 481 rpsgm]d]s]v]l]c]e]y]d]a]g]a]c]a]w]e]l]t]p]a]e]t]v]r]l]r]a]y]l]n]t]p]g]l]v]c]q]d]h]e]f]w]e]s]v]t]g]t 540
DB 578 h]d]a]h]t]s]q]t]k]g]a]g]d]n]f]p]y]l]v]a]y]a]t]v]c]a]r]a]q]a]p]p]s]w]d]g]m]w]k]c]i]r]l]k]p]t]l]h]g]p]p]l]y 637
QY 541 h]d]a]h]t]s]q]t]k]g]a]g]d]n]f]p]y]l]v]a]y]a]t]v]c]a]r]a]q]a]p]p]s]w]d]g]m]w]k]c]i]r]l]k]p]t]l]h]g]p]p]l]y 600
DB 638 r]l]g]a]v]g]n]e]i]t]t]h]p]i]c]k]f]y]m]a]c]m]s]a]d]l]e]v]t 668
QY 601 r]l]g]a]v]g]n]e]i]t]t]h]p]i]c]k]f]y]m]a]c]m]s]a]d]l]e]v]t 631

DE

RESULT 32
ID R53417 standard: Protein; 3010 AA.
AC R53417;
DT 17-JAN-1995 (first entry)



(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_nu n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Aug 26 09:12:13 1997; MasPar time 2128.91 Seconds
1172.094 Million cell updates/sec

Tabular output not generated.

Title: >US-08-292-694A-3
Description: (1-2272) from US08292694A.seq
Perfect Score: 2272
N.A. Sequence: 1 CACGCGCGCGCATGAGCTG.....CTTCCACACACTGTGGCA 2272
Comp: GTGCGCGCGGCTACTGAC.....GANAAGTGTGACACCCG

Scoring table: TABE default

Gap 5

Match STD : Dbase 0; Query 0

Searched: 362067 seqs, 549138275 bases x 2

Post-Processing: Minimum Match 0%

Listing first 45 summaries

Database:

Database:

genbank99

18:BC11 19:BC12 20:BC13 21:BC14 22:BC15 23:BC16 24:BC17
25:BC18 26:BC19 27:BC10 28:BC11 29:BC12 30:BC13
31:GEN3 32:HTG1 33:HTG2 34:HTG3 35:INV1 36:INV2 37:INV3
38:INV4 39:INV5 40:INV6 41:INV7 42:INV8 43:INV9 44:INV10
45:INV11 46:MAM1 47:MAM2 48:MAM3 49:VRT1 50:VRT2 51:VRT3
52:VRT4 53:PAT1 54:PAT2 55:PAT3 56:PAT4 57:PAT5 58:PHG
59:PLN1 60:PLN2 61:PLN3 62:PLN4 63:PLN5 64:PLN6 65:PLN7
66:PLN8 67:PLN9 68:PLN10 69:PR11 70:PR12 71:PR13
72:PR14 73:PR15 74:PR16 75:PR17 76:PR18 77:PR19
78:PR20 79:PR21 80:PR11 81:PR12 82:PR13 83:PR14 84:PR15
85:ROD1 86:ROD2 87:ROD3 88:ROD4 89:ROD5 90:ROD6 91:ROD7
92:ROD8 93:STR 94:STR 95:DNA 96:VRL1 97:VRL2 98:VRL3
99:VRL4 100:VRL5 101:VRL6 102:VRL7 103:VRL8 104:VRL9
105:VRL10

Database:

genbank-new3

106:BC1 107:GEN1 108:GEN2 109:HTG1 110:HTG2 111:INV
112:MAM 113:VRT 114:PHG 115:PLN 116:PR1 117:PR2
118:ROD 119:STR 120:DNA 121:VRL
u-emb150_99
122:part1

Database:

Statistics: Mean 12.005; Variance 5.716; scale 2.100

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	2272	100.0	2272	88	MUSDELOPRE	Mouse delta opioid re	0.00e+00
2	2095	92.2	2203	92	S6181	delta opiate receptor	0.00e+00
3	2053	90.4	2219	88	MUSDELTO	Mus musculus delta-op	0.00e+00
4	1705	75.0	1834	92	S65335	delta opioid receptor	0.00e+00
5	1705	75.0	1835	88	MUSDOPRCP	Mouse delta-opioid re	0.00e+00
6	1124	49.5	1366	92	RNU00475	Rattus norvegicus Spr	0.00e+00
7	1119	49.3	1418	91	RATRORA	Rat mRNA for rat opio	0.00e+00
8	889	39.1	1773	77	HSU07882	Human delta opioid re	0.00e+00
9	878	38.6	1136	77	HSU10504	Human delta opiate re	0.00e+00
10	552	24.3	685	48	SSU71149	Sus scrofa delta opio	0.00e+00
11	365	16.1	1401	91	RATMOPIOLD	Rat mu opioid recepto	5.32e-282
12	365	16.1	1448	92	RATMO2083	Rattus norvegicus mu-	5.32e-282
13	365	16.1	1586	91	RATMORA	Rattus norvegicus mu	5.32e-282
14	363	16.0	2135	91	RATMOR1A	Rattus norvegicus Mu	3.10e-280
15	361	15.9	2397	91	RATRORB	Rat mRNA for rat opio	1.81e-278
16	359	15.8	1367	92	MUS3424	Rattus norvegicus mu	1.06e-276
17	357	15.7	1610	87	MUS28915	Mus musculus mu opioi	6.10e-275
18	354	15.6	356	92	S81965	delta opioid receptor	2.73e-272
19	354	15.6	145	112	BTU89677	Bos taurus mu opioid	2.73e-272
20	354	15.6	145	10	BTU89677	Bos taurus mu opioid	2.73e-272
21	355	15.6	2229	87	MU019380	Mus musculus mu opioi	3.58e-273
22	348	15.3	2302	48	PIGMOPR	Homo sapiens (clone 1d7	3.57e-267
23	338	14.9	1610	82	HUMOP10DA	Homo sapiens opioid r	3.50e-258
24	336	14.8	1473	77	HSU12569	Human mu opiate recep	2.02e-256
25	336	14.8	2162	82	HUMOR1X	Human mu opiate recep	2.02e-256
26	326	14.3	2205	48	SSU72758	Sus scrofa orophant F	1.29e-247
27	321	14.1	1252	82	HUMOPRLP	Homo sapiens (clone A	3.22e-243
28	321	14.1	1973	75	HSOR11	H. sapiens mRNA for OR	3.22e-243
29	321	14.1	2534	77	HSU30185	Human orphan opioid r	3.22e-243
30	303	13.3	1154	77	HSU17298	Human kappa opioid re	2.08e-227
31	303	13.3	1604	82	HUMOPR1B	Homo sapiens (clone d	1.08e-227
32	301	13.2	1182	77	HSU11053	Human kappa opioid re	1.18e-225
33	295	13.0	720	92	S77863	mu-opioid receptor MO	2.16e-220
34	291	12.8	1288	92	S81111	kappa opioid receptor	6.90e-217
35	291	12.8	1410	89	MUSKAPOPRE	Mouse kappa opioid re	6.90e-217
36	286	12.6	1733	85	CPU04092	Cavia porcellus Hatt1	1.65e-212
37	282	12.4	1253	91	RATOPRE	Rattus norvegicus opi	5.22e-209
38	282	12.4	1452	92	RNU01913	Rattus norvegicus Spr	5.22e-209
39	282	12.4	1567	91	RATOPRECEP	Rat opioid receptor f	5.22e-209
40	282	12.4	1817	91	RATRORC	Rat mRNA for opioid r	5.22e-209
41	282	12.4	2354	92	RNU07871	Rattus norvegicus Spr	5.22e-209
42	282	12.4	2706	91	RATXOR1A	Rattus norvegicus alt	5.22e-209
43	279	12.3	1358	90	RATXOR1A	Rat kappa opioid rece	2.19e-206
44	279	12.3	2094	90	RATXOR1B	Rattus norvegicus kap	2.19e-206
45	279	12.3	2481	90	RATXOR	Rattus norvegicus mRN	2.19e-206

ALIGNMENTS

1 MUSDELOPRE 2272 bp mRNA ROD 13-DEC-1993
DEFINITION Mouse delta opioid receptor mRNA, complete cds.
ACCESSION L11064
NID g348246

KEYWORDS delta opioid receptor.
SOURCE Mus musculus (library: Clontech #ML1036a) brain cDNA to mRNA.
ORGANISM Mus musculus

Eukaryotes; mitochondria; eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
1 (bases 1 to 2272)

REFERENCE
1 Yasuda,K., Raynor,K., Kong,H., Breder,C.D., Takeda,T., Reisine,T.
and Bell,G.I.
Cloning and functional comparison of kappa and delta opioid

receptors from mouse brain
proc. Natl. Acad. Sci. U.S.A. 90, 6736-6740 (1993)

FEATURES

1..2272 Location/Qualifiers
/organism="Mus musculus"

Query Match	100.0%	Score 2272;	DB 88;	Length 2272;
Best Local Similarity 100.0%;	Pred. No. 0.00e+00;	Mismatches 0;	Indels 0;	Gaps
Matches 2272;	Conservative			
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61	tcaactctcggaagcctctcccaagcctctcccaagcgcgaggcgcaatgtgtgggt	120	12..1130	
61	TCAACTCTCGGAAGCCTTCCAGCCCTTCCAGCCCTTCCAGCGGGCGCAATGCTGGGGT	120	/codon_start=1	
121	cgcgggagcccgtaagtcctctgcccctgcccctagcaatcgccatcacccgcctact	180	/product="delta oploid receptor"	
121	CGCGGAGCCCGTAAGTCCTCTGCCCTGCGCTTACCATCGCATACCGCGCTTACT	180	/db_xref="pid:g348247"	
181	cggctgtgtgcagttgagggtgttccttgaggcaagctgtcgtcatgltttggcatcgttcgt	240	/translation="MEIVPSARAEIQQSPVNIISDAPSPAPSPGAGAGSGPGA	
181	CGGCTGTGTGCAGTTGAGGTTCTTGGGCAACGGCTCGCATGTTGGCATCGTCGGT	240	SLALAIATLTSAYCAVGLGNVIMVGMGYIRTKLTATNTIIFNLALADALA	
241	acaccaaatgaaagacgcgcacaacatctacatcttcaatctcgtgcttggctgtagtcgc	300	PRQSAFLMEIWFPEFELICAKLSIDYNNMTSLFLTMMSSVDYTIACVHPVA	
241	ACACCAAAITGAAGACGCGCCACACACTCATCTTCATCTGGGTTTGGCTGATGCGC	300	TKAKALINICIMVILWASGVYVIMVMTATPQDPAVAGLOFSPSPVMTQVKA	
301	tggccacacgaagcctccctccagagcgccaagtaactgatggaagaagtggcgcttg	360	LEAFVPLIITFYCYGKMDRLRLRSVRLISGKEDRSIRTRITAVILVGAFAVYK	
301	TGGCCACACGAAGCCTGCCCTCCAGAGCGGCAAGTACTTGATGGAAAGCTGGCGTTG	360	ITFFVYMTVILINDRDLVVAALHICAIYGAANSNPVLYATLDENKRCFR	
361	gcgagctcgtgtgcaagcgtgtgctcccatctgactactacaacatgcttaactagcatct	420	TCGRQPSLSLRPQATTRVYACTPDSRGGGAAA"	
361	GCGAGCTCTGTGCAAGCCTTGCTTCACATGTGACTCATCAACATGTCACATGACTG	420		
421	tcaccctccacatgatgagcgttggacgcgtacatctgctctgtccatctcttcaaaagcc	480		
421	TCACCCTCACCATGATGAGCGCTGGACCGCTCATTTGCTGCTCCATCCCTGTCAAAGGCC	480		
481	tggacttcgcgaacacacacgaagcgcaagctgatacatatgacatgtggtcttgct	540		
481	TGGACTTCGCGACACACACCAAGCGCAAGCGAAGCATTAATATGATCTTGGGCTT	540		
541	caggtgtcgggggttcccatcaatgtgcatgtgcagtgcagtcacaccccggaatgtgtcagttg	600		
541	CAGGTGTGGGGTCCCATCAATGTGCAATGAGGAGACCAACCCCGGAAGTGTGCAGTGG	600		
601	tatgatagtccagttcccaagctcccaagctgttactcttgggaactgtgtacaagaatctgcg	660		
601	TATGATAGTCCAGTTCGCCCATGCTCCCAATCGTACTGGGACACTGTGACCAAAATCTGGG	660		
661	tggtcctcttgccttctgtgtgtgcgcagatccctacatcaacaggtgtgtatgagctatag	720		
661	TGTTCTCTTTCCTCTCGTGGGCGCATCCATCATCACGCTGTGCTATGCGCTCATGG	720		
721	tactgagctgtgcagcgtgtgctgtgtcgttcacgggttccaaagaaagacagcgagctgcg	780		
721	TACTGAGCTGTGCAGCGTGTGCTGTGTCTGCTGCTCGGTTCCAAAGAAAGACGACGCTGC	780		
781	ggcgatacagcagatgt	840		

QY	781	GGGCATACCGCATG	TGCTGCTGGGGTGGTGGGGCCTTG	TGGTGGCTGGGGGCCCA	840
Db	841	tcacatcttcgtca	tgcgtctggagcgtgtgtggacatcaatc	gcgcgcgaaccactt	900
QY	841	TCCACATCTTGCTG	CTGCTGTGGAGGCTGGTGGATCAATCAATCGGGCCACCACTTG	GGG	900
Db	901	tggcgacatc	acacttgcacattggcgtcgtgtacgcacaagcagcctcaaccggttc		960
QY	901	TGGCGCACTGCACT	GTGTGCACTTGGCGCTGGGCTACGCCAACAAGCAAGCCTCAACCGG	GTTC	960
Db	961	tctacgcttcct	gtgacgagaaatcaacgctgtcttcgcgcagctctgtgcagccct		1020
QY	961	TCTACGCTCTCTG	AGCAGAACTTCAAGCCGCTGCTCCGACAGCTCTGTGCGACG	CCCT	1020
Db	1021	ggcgccgcgaaga	aacccggaagtctccgttcgtcccgccagggccacgcacgcgttgaagctg		1080
QY	1021	GGGCGCGCAAAAC	CCCGGCACTTCGCTGCTGCCCGCCAGGCCACACGCTGAGCTTG		1080
Db	1081	tcaactgcctc	acccctctcgcacgcgcggcggtgtgcgtctgcgccttacaccgcac		1140
QY	1081	TCACTGCTGCAC	CCOCTCCAGCGCCGGGGTGGCGCTGC	CGCCTACCCGAC	1140
Db	1141	cttcacctaaac	gcccctctcccaagtgaagtatccagagggccacaacccgaatctccctg		1200
QY	1141	CTTCCCTTAAAC	GGCCCCCTCCAGTGAAGTATCCAGAGGCCACACCAAGCTCCTTG		1200
Db	1201	aggcgtgtgcca	ccaccacagagcagctagaaattgggcgtcacagagggagagcctcctgt		1260
QY	1201	AGGCTGTGGCCAC	CAACCAGGACGCTAGAAATTGGGCTCCACAGAGGGAGGCTCCTCT		1260
Db	1261	gggagcgggcct	gtgaagatcaaaagctccaaagttagaaacgtgtggaggtgaggaagcaga		1320
QY	1261	GGGAGCGGGCCT	GTGAGGATCAAAAGGCTCCAGGTTGGAACGGTGGGGGTGAAGAAACAA		1320
Db	1321	gctgtgattct	ctaacttataccttataagagtcctctccatgtggaagagccctccgc		1380
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DEFINITION Mus musculus delta-opioid receptor mRNA, complete cds.
ACCESSION L06322
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SOURCE Mus musculus cDNA to mRNA.
ORGANISM Mus musculus
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
REFERENCE 1 (bases 1 to 2219)
AUTHORS Kieffer,B.H., Beifort,K., Gaveriaux-Ruff,C. and Hirth,C.G.
TITLE The delta-opioid receptor: Isolation of a cDNA by expression cloning
and pharmacological characterization
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89, 12048-12052 (1992)
MEDLINE 93101664
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SOURCE mice NG108-15 cells.
ORGANISM Mus sp.
REFERENCE 1 (bases 1 to 1834)
AUTHORS Keith,D.E., Jr., Anton,B. and Evans,C.J.
TITLE Characterization and mapping of a delta opioid receptor clone from
NG108-15 cells
JOURNAL Proceedings of the Western Pharmacology Society 36, 299-306 (1993)
MEDLINE 93391482
REMARK GenBank staff at the National Library of Medicine created this
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This sequence comes from Fig. 1.
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 Murinae; Rattus.
 REFERENCE 1 (bases 1 to 1366)
 Aboud, M.E.
 AUTHORS Molecular cloning and expression of a rat delta opioid receptor
 TITLE from rat brain
 JOURNAL J. Neurosci. Res. 27, 714-719 (1994)
 REFERENCE 2 (bases 1 to 1366)
 Aboud, M.E.
 AUTHORS Direct Submission
 TITLE Submitted (09-AUG-1993) Mary E. Aboud, Pharmacology and Toxicology,
 Medical College of Virginia/Virginia Commonwealth University, 1112
 F. Clay St., Richmond, VA 23298, USA
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 LOCUS RNU00475 1366 bp mRNA 22-UTL-1994
 DEFINITION Rattus norvegicus Sprague-Dawley delta opioid receptor (dori) mRNA,
 complete cds.
 ACCESSION U00475
 NID 9403488

KEYWORDS G-protein coupled receptor; rat opiod receptors; transmembrane protein..

SOURCE Rattus norvegicus (strain Wistar) adult brain cDNA to mRNA, clone PRO10.

ORGANISM Rattus rattus

REFERENCE Eukaryotic: mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae, Rattus.

AUTHORS 1 (bases 1 to 1418)
Fukuda,K., Kato,S., Mori,K., Iwabe,N., Miyata,T., Nishi,M. and Takeshima,H.

TITLE Primary structures and expression from cDNAs of rat opiod receptor delta- and mu-subtypes

JOURNAL FEBS Lett. 327, 311-314 (1993)

MEDLINE 93351652

REFERENCE 2 (sites)

AUTHORS Wang,J.B., Johnson,P.S., Imai,Y., Persico,A.M., Ozenberger,B.A., Eppler,C.M. and Uhl,G.R.

TITLE CDNA cloning of an orphan opiate receptor gene family member and its splice variant

JOURNAL FEBS Lett. 348, 75-79 (1994)

MEDLINE 94298959

COMMENT Submitted (03-JUN-1993) to DDBJ by: Hiroshi Takeshima International Institute for Advanced Studies
c/o Shimadzu Corporation N-80
1 Nishinokyo-Kuwarehara-cho
Kyoto 604
Japan
Phone: 075-823-1208
Fax: 075-811-8185.

FEATURES

Source location/Qualifiers

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 DEFINITION Human delta opioid receptor mRNA, complete cds.
 ACCESSION U07882
 NID 9497313
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 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 1773)
 AUTHORS Knapp, R.J., Malatynska, E., Fang, L., Xiaoping, L., Nguyen, M., Santoro, G., Varga, E.V., Hruby, V.J., Roeseke, W.R. and Yamamura, H.I.
 TITLE Identification of a human delta opioid receptor: Cloning and expression
 JOURNAL Life Sci. 54, PL463-PL469 (1994)
 MEDLINE 94260835
 REFERENCE 2 (bases 1 to 1773)
 AUTHORS Knapp, R.J.
 TITLE Direct Submission
 JOURNAL Submitted (21-MAR-1994) Richard J. Knapp, Pharmacology, The University of Arizona College of Medicine, Tucson, AZ 85724, USA
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 LOCUS HSU10504 1136 bp mRNA PRI 16-DEC-1995
 DEFINITION Human delta opiate receptor mRNA, complete cds.
 ACCESSION U10504
 NID 9501144
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 1136)
 AUTHORS Simonin, F., Befort, K., Gavériaux-Ruff, C., Mathes, H., Nappay, V., Lannes, B., Michelletti, G., and Kieffer, B.
 TITLE The human delta-opioid receptor: genomic organization, cDNA cloning, functional expression, and distribution in human brain
 JOURNAL Mol. Pharmacol. 46 (6), 1015-1021 (1994)
 MEDLINE 95107267

ORIGIN	Query Match	Score	DB	Length
Best Local Similarity	24.38	552	48	686
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Matches 619; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

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ACCESSION J22455
NID 9437671
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SOURCE Rattus norvegicus (strain Sprague-Dawley) cDNA to mRNA.
ORGANISM Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 1401)
AUTHORS Thompson R.C., Mansour A., Akil H. and Watson S.J.
TITLE Cloning and pharmacological characterization of a rat mu opioid receptor
JOURNAL Neuron 11 (5), 903-913 (1993)
MEDLINE 94039560
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location/Qualifiers
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	SOURCE		Norway rat.				
	ORGANISM		Rattus norvegicus				
	REFERENCE		Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrates; Rutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Rattus.				
	AUTHORS		Bunzow,J.R., Zhang,G., Bouvier,C., Saez,C., Ronnekley,O.K., Kelly,M.J. and Grandy,D.K.				
	TITLE		Characterization and distribution of a cloned rat mu-opioid receptor				
JOURNAL			J. Neurochem. 64 (1), 14-24 (1995)				
MEDLINE			95096825				
REFERENCE			2 (bases 1 to 1448)				
AUTHORS			Bunzow,J.R.				
TITLE			Direct Submission				
JOURNAL			Submitted (24-SEP-1993) James R. Bunzow, VIABR, Oregon Health Sciences University, 3181 S.W. Sam Jackson Park Rd., Portland, OR 97201 USA				
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Matches 623; Conservative			0; Mismatches 240; Indels 3; Gaps 2;				
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444	GACCGCTACATTGCTCTCGGCCATCCTGTCAAGCCCTGGACTTCGGACACACAGCCAG	503											
760	gccaaatcgtcaagctcgtcaactgattccctctctctgcatcagtgctgctgtaag	819											
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940	cgcattccatcatactactgtgtttagcggccctgattatctttagcactcaagaagcgttcg	999											
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1177	gcttgggtgttaacgaaacagctgctgtgaatccagttctttagcctctcctgataaag	1236											
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RESULT 13													
LOCUS	RATMORA	1586 bp	mRNA	ROD	03-AUG-1993								
DEFINITION	Rattus norvegicus mu opioid receptor mRNA, complete cds.												
ACCSSION	L13069												
NID	9348250												
KEYWORDS	mu opioid receptor.												
SOURCE	Rattus norvegicus												
ORGANISM	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Rattus.												
REFERENCE	1 (bases 1 to 1586)												
AUTHORS	Chen,Y., Meslek,A., Liu,J., Hurley,J.A. and Yu,L.												
TITLE	Molecular cloning and functional expression of a mu-opioid receptor from rat brain												
JOURNAL	Mol. Pharmacol. 44, 8-12 (1993)												
MEDLINE	93341493												
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BASE COUNT 376 a 479 c 361 g 370 t

ORIGIN

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 ETAAFLP"

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CC receptor proteins, for use in diagnosis, drug design and therapeutic applications.
CC Sequence 2272 BP: 485 A; 665 C; 650 G; 472 T;
Query Match 100.0%; Score 2272; DB 13; Length 2272;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 2272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 181 cggctgtgtgcagtgagggtgtctctggtgcaacgtgtcgtatgtttggcaatcgtccggt 240
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Db 721 tactgcgctcgcgaagcgatgctgtctgtctgcggttccaaggaagaagacgcgacgtgc 780
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Db 1141 ctccctttaaagccctcccaagtgaatgatacagaagggccacacaggtccctcgtg 1200
QY 1141 CTCCCTTTAAAGCCCTCCCAAGTGAATGATTCAGAGGCCACACCGACTCTCTGGG 1200

Db 1201 aggtgtgcccacacagaagacaagtgaattgggctctgcacaagggagggccctctgt 1260
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Db 1801 ctgggcaatttagtgctcaaatataaatgtaagaagggctggygaatgtaagctgagtg 1860
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Db 1981 tgaagagaacccgcagccctgtatccctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2040
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QY 2101 TAAGCCTTGTGTCAAGAAGTGGAGTAGAACCAAGAAAGTGGCTGAGTGATTAAGGGCA 2160
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RESULT 2
ID Q6656 standard; cDNA; 2216 BP.
AC Q6656;
DE 19-JAN-1995 (first entry)
KM Murine delta opioid receptor coding sequence.
KW delta opioid; enkephalin; receptor; mouse; murine; analgesic; pain;
OS drug addiction; neurological disorder; psychiatric; disorder;
KW cardiovascular disorder; ds.
OS Mus musculus.
FH Key Location/Qualifiers
FH CDS 59..1174
FT /*tag= a
FT /product= opioid_receptor
FN FR2697850-A.
PD 13-MAY-1994.
PF 10-NOV-1992; 013526.
PR 10-NOV-1992; FR-013526.
PA (UTST-) UNITV PASTEUR STRASBOURG LOUIS.
PI Kieffer B;
PI WPI; 94-178255/22.
DR P-PSDB; R66503.
PT New nucleic acid encoding opioid receptor - and related
PT polypeptide, antisense nucleic acid, probes, recombinant cells
PT and ligands, useful in diagnosis and treatment of e.g.
PT neurological disorders
PS Claim 3; Page 16-18; 29pp; French.
CC A cDNA bank constructed from hybridoma NG108-15, was used to
CC transfect COS-1 cells. The cells were tested for ability to bind
CC tritium-labelled Tyr-D-Thr-Gly-Phe-Leu-Thr, in the presence or
CC absence of the opioid antagonist naloxone. Clone K56 was isolated
CC from a positive colony and found to contain a 2216bp insert. This
CC cDNA encodes a delta opioid (enkephalin) receptor with apparent
CC dissociation constant 1.4nM and Bmax 3.9-6.4 pmole/mg protein.
SQ Sequence 2216 BP; 460 A; 647 C; 649 G; 460 T;

Query Match 89.4%; Score 2032; DB 11; Length 2216;
Best Local Similarity 98.8%; Pred. No. 0.00e+00;
Matches 2142; Conservative 0; Mismatches 8; Indels 17; Gaps 7;

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DB 111 acctctggaaccccttccacagcgcctccacagcgcgcgcaaatgctgtgggtgtgc 170
QY 64 ACGCTCGAGACCCCTTTCCACAGCCCTTCCACGCGGGGCCCATGTGGGGGTGC 123
DB 171 cgggagcccgtagtgcctgcctgcctgcctgacatgcacatcacgcgcgtctactcgg 230
QY 124 CGGGAGCCCGTAGTSCCTGCTCCCTGCGCCATGCGCATACCGCGCTCTACTCGG 183
DB 221 ctgtgtgagcagtggtgggtcttctggcacaagcgctgcatagtttgggaatgcgtac 290
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QY 244 CCAATTTAAGAACCCGCCCAACATCTACATCTTAATCTGGCTTGGCTGATGGCTGG 303

DB 351 ccaacagcagctgcccctccagagcgccaggtactgtatggaaaagtgccgtttggg 410
QY 304 CCACACAGACGCTGCCCTTCCAGAGCGCAATACTTATGTGAACGTGGCCGTTGGG 363
DB 411 agctgtgtgaaggctgtgtctctccattgactaactacacatgttctactacatctca 470
QY 364 AGCTGCTGTGAAGGCTGTGCTTCATGTACTACTACACATGTTCACTACATCTTCA 423
DB 471 cctcaacatgtagcgtgtgacgcgtacattgcgtctgcatacctcgtcaaaagccctgg 530
QY 424 CCGCTCAACATGATGAGCGGTGACCCGCTACATGTGCTGTGCAATCCTGCAAAAGCCCTGG 483
DB 531 acttccggac 590
QY 484 ACTTCGGAC 543
DB 591 gttcggggtccac 649
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QY 1324 GGTGATTCTTAAGTGTATCATTAAGTAAGAGCTCTCCAAATGGGAGACAGAGCTCCGCTT 1383

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Q	y	1384	GAGATACATCGGGTTCTGCCCCAAAAGAACC-AGCTCCAGTCCAAGACCAAGATT	1442
D	b	1488	ccaactccagaagcaccaaggagggcagtgtgatggctcgatgatgttggttgctgaagtc	1547
Q	y	1443	CCAGCTCCAAAGAACCAAGAGGG-----TCGATGATTGGTTGGCTGAGATC	1491
D	b	1548	ccaagatttgttaatgagggagatctccatcttagagaagaataaggagcaaggcat	1607
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D	b	1668	taagtggggagtgtcaactgttagagaagatcaaatgttccacaacctttaactact	1727
Q	y	1612	TAAATGGGGGATGCTCACGTTTGGAAGAAGTCAAAGTTCTACACACTTCTAACTACT	1671
D	b	1728	caagctaactcgtttgaggtcgaaggccaagctgactctctgtagaagagatacaagcgg	1787
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D	b	1788	gctgtatggggcagcgctgtgtatcccagtcacatagtggaagctgaagctggaataaa	1847
Q	y	1731	GCTGATAGGGGCAAGGC-TGTGTATCCCAAGTCAATGAGAGGCTGAGGCTGAAAAATTAA	1789
D	b	1848	ggaccaacagccctggggcaatttagtgttccaataaataatgaagaagaggtcgggaagt	1907
Q	y	1790	GGACCAACAGCTGGGCATTTAGTGTCTCAAAATTAATGTAAAGAGGCTGGGAATGT	1849
D	b	1908	agctcagctgttaggtgtgtttgtgttgaggtcgtggaatcaataaga caaacaacaaca	1967
Q	y	1850	AGCTCATGTGTAAGGCTTGTGTGTGAAGGCTCTGGATCAATAAACAACAACAACA	1909
D	b	1968	accaaaaacctccaacaacaacaaccccaacctcaacaacaanaaactatgtgtgtctc	2027
Q	y	1910	ACCAAAAACCTTCCAAAACAACAACAACCAACCTCAACCAAAAAAACTATGTGGTCTC	1969
D	b	2028	tgaatcgtgttgaagaaagacccgcagccctgfatccctgtgtgggtgtgagcaatggc	2087
Q	y	1970	TGAATCTGGTTTGAAGAACAACCGCAACCTGTATCCCTGTGGGCTGTGGCAATGGGC	2029
D	b	2088	agaagcagagagctcccccgtgatctctgaacaagggccccaaaagaagcttcaaggacc	2147
Q	y	2030	AGAAGCAGAGGCTCCCTCGATCTCTGAACAAGGGCCCCAAAAGCAATTTCTAAGGACCC	2089
D	b	2148	ctgaaccagagtaaagccttctgtgtcaagaagtggagatcaaccagaaagtgtgctgagt	2207
Q	y	2090	CTGAACAACGAGATAGCCTTGTGTGAAGAAGTGGAGTGAACCAAGAAGGTGCTGAGT	2149
D	b	2208	gctttag 2214	
Q	y	2150	GATTAG 2156	

RESULT 3
ID Q56700 standard; cDNA; 1821 BP.

AC Q56700; 15-SEP-1994 (first entry)

DE Sequence of murine delta opioid receptor in the DOR-1 cDNA clone.

KW Opioid receptor; morphine; opiate; ss.

OS Mus musculus.

EH key Location/Qualifiers

FT CDS 29..1139

FN /tag= a

PN W09404552-A.

PD 03-MAR-1994.

PE 13-AUG-1993; U07665.

FR 13-AUG-1992; US-929200.

RA (REGC) UNIV CALIFORNIA.

PI Edwards RH, Evans CJ, Kaufman D, Keith DE;

DR NPf: 94-083099/10.
PT P-PSDB: R48629.
DR DNA encoding opioid receptors and antibodies against this
PT receptor - used to express and locate these receptors, and screen
PT cpts. for opioid (ant)agonist activity
PS claim 1: Fig 5: 74pp: English.
CC A cDNA library was constructed using mRNA isolated from the NG109-15
CC cell line. A single clone, named the DOR-1 clone was isolated.
CC Comparisons with known sequences in GenBank showed highest homology
CC between DOR-1 and the G-protein-coupled somatostatin receptor. Other
CC features of the DOR-1 clone AA sequence deduced from the cDNA
CC sequence include 3 consensus glycosylation sites at residues 18 and
CC 33 (predicted to be in the extracellular N-terminal domain), and at
CC residue 310 (close to the C-terminus and predicted to be
CC intracellular). Phosphokinase C consensus sites are present within
CC predicted intracellular domains, at residues 242,255, 344 & 352.
CC Seven putative membrane-spanning regions were identified. The DOR-1
CC clone produces a delta receptor with a predicted mol. wt. of 40,558
CC kdaltons prior to post-translational modifications.
SQ Sequence 1821 Bp: 339 A: 359 C: 362 T:

Query Match	71.7%;	Score 1629;	DB 10;	Length 1821;
Best Local Similarity	98.2%;	Pred. No. 0.00e+00;		
Matches 1781; Conservative	0;	Mismatches 8;	Indels 24;	Gaps 13;

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Db	81	aacctctgagagcctctccagagcctctcccaagcgagcgccaatgctgctcgaggtgc	140
QY	64	ACCTCTGGAGAGCCTTCCAGAGCCTTCCAGAGCGGAGGCGCAATGCGTGGGGGTGC	123
Db	141	cgagagcccgtagtgcctgtccctgcacctagccaagccaacacgagcgtctactcgg	200
QY	124	CGGAGGCCGTAAGTGGCTCTCCCTCGCCCTGACCATGCCATCCAGCGGCTCTATCCG	183
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QY	244	CCAATTGAAGACGCCACCAACATCATCTTAATCTGTGCTTTGGCTATGACGCTMG	303
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QY	484	ACTTCGGAACACCGCAAGGCCAAGCTGATCAATATGATCGGGTCTTGGCTTAG	543
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QY	544	GTGTGGTGGTCCCATATGTATGTATGTGACATGTGACCCACCCCGGATGTATGATGTAT	603
Db	621	gaatgtccaaatctcccaagtcacagctgtaactggtgagacactgtgacaaagatctgtcgtt	680
QY	604	GAATGTCCAAATCTCCCAAGTCCAGTCCAGTGTGAGTGGACACTGTGAACAAGATCTGCTGT	663
Db	681	tccctttgctctgtgtgtgcagatcctcaatacaacggtgtgtcatggtcctatgctaac	740
QY	664	TCCCTTTGCTCTGTGTGTGCAGTCTCATATCAAGGTGTGCATGTGCCCCATGCTAC	723

[illegible]

QY	1792	ACCAACAGCCCTGG	1804
RESULT	4		
ID	089223	standard;	CDNA; 1618 BP.
AC	089223;		
DT	20-OCT-1995	(first entry)	
DE	Transcription regulatory protein cDNA.		
KW	Mu oploid receptor; MOR-1; gene therapy; diagnostic;		
OS	transcription regulatory protein; ss.		
FS	Rattus sp.		
FT	Key	Location/Qualifiers	
FT	CD5	339..1235	
FT	/*tag= a		
PN	W09307985-A.		
PD	23-MAR-1995.		
PE	13-SEP-1994; U10358.		
PR	13-SEP-1993; US-120601.		
PA	(INDV) UNIV INDIANA FOUND.		
PI	Yu L;		
DR	WPI; 95-131351/17.		
DR	P-P5DB; R71965.		
PT	New nucleic acid encoding new human mu oploid receptor - and		
PT	related vectors, transformed cells, antibodies etc., useful in		
PT	diagnosis, treatment and drug screening.		
PS	Disclosure; Page 199-203; 266pp; English.		
CC	A 365 bp fragment of the mouse delta oploid receptor was used to		
CC	screen a rat brain cDNA library under low stringency conditions.		
CC	One positive clone included the sequence given in 089222, encoding a		
CC	mu oploid receptor, MOR-1 (R71964). Sequence analysis revealed an		
CC	alternative reading frame (089223) encoding a zinc		
CC	finger-containing transcription regulatory protein (R71965).		
CC	Sequence 1618 BP; 390 A; 486 C; 370 G; 372 T;		

Query Match	16.1%;	Score 365;	DB 14;	length 1618;
Best Local Similarity	71.9%;	Pred. No. 9,92e-226;		
Matches	623;	Conservative	0;	Mismatches 240;
			Indels	3;
			Gaps	2;

Db	403	tcacatggtcaaacacacattacacaaacagggccctactactatcgltgtgtatgaggctc	462
QY	144	TCcctGGccctTACCcATTCGccATTCACccCGGcCTTCATCGcCTGTGTGTccCATGTGGGGcTT	203
Db	463	ttcggaactctccgtgtcatgltatgltatgattgttaagatacaccacaaatgaagatgcacc	522
QY	204	CTGGGCAACCTGGCTGCTGATGTTTGGACATCGCGGTACACCAATTGAAAGCCGCCACC	263
Db	523	aaatcttaattttaacttgcctctgtggagaagccttagagaacaaagtaactgccttt	582
QY	264	AAcATCTACATCTTCATATGTGGTTGGGTGTATGGCTGTGCACCGACACGCTGTCCCTTC	323
Db	583	cagaagtcaactaactgtatgggaacatgagcccttcggaaacatctctctgaaagtctg	642
QY	324	CAGAAGGCCAAGACTTGATGGAAGCTGGCCGTTTGGCGAAGCTGCTGTGCAGAGCTGTG	383
Db	643	atctcaatgattactacacaaatgttcacaaagacataatccactcttgcacaaatagcgtg	702
QY	384	CTCTCCATTTGACTACTACAACTAGTTTCATCTACCAACTTTCACCTTACCATATGAGCGTG	443
Db	703	gaacgctacaatgctgtctgtgccaccacgtcaaaagcctgagatttcogtatccccccgnaat	762
QY	444	GACCGGTAACTTGTCTGTCCCATCTGTCAAAAGCCCTGGAACTTCCGAGACACCAACGAA	503
Db	763	ggcaaatatgtaangtctgcgaactgagatccctctttcgcatactggtcgtcgtgtaatg	822
QY	504	GCCAACTGATCAATTAATATGACTCTGGGGCTCTTGGCTTAAGTGTGGGGGTCCCATCTATG	563
Db	823	ttcatgtgcaacacaaatatagcaggcgaaggtgtccatagatatggcacccctaagctttccaac	882
QY	564	GTCATGGCAGTGAACCAACCCCGGGAGTGGTAGAGTGATGTGATCTCCAGTTCGCCCGAT	623
Db	883	ccaactgttactgggagaaactgctcaaaatctgtgtcttatacttcgtgttcaatcatg	942

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QY 624 CCCAGCTGGTACTGGGAACTGTGACCAAGATCTGGCTGTTCTCTTGGCCTTGCTGTG 683
Db 943 cgcgactcctacatcaactggtgtgttaacgacctgatatgacttaacgaatgaagcttcgc 1002
QY 684 CGGATCCGATCATCAACAGGCTGTGATGAGCTCATGTGACTAGCGGCTGCGGAGGCTGGT 743
Db 1003 atgctatcggctcccaagaagaagaacgaatctgcgcagatcaaccggatggtctg 1062
QY 744 CTGGCTGCTCCGGTTCCAAAGAGAGACCGGACCTCGGCGCCATCCAGCTGATGCTGG 803
Db 1063 gtgtctgtggtgtattatattatgctgtcgtgaccccccatccacatctgaatcatcaaa 1122
QY 804 GTGGTGGTGGGCGCCTTGCTGTGCTGTGGCGCCCATCCATCTTCATCTGATGCTGG 863
Db 1123 cgcgtgtatc-acg--attccagaacaacacatttgaacgctttcctggaacttgcatt 1179
QY 864 ACGGTGGTGGACATCAATCGCGGAGACCACTTGGTGGCGGACATCGACCTGGCATTT 923
Db 1180 gctttgggttacacgaacagctgacctgaatccagttcttaccgcttccctggtgaaac 1239
QY 924 GCGCTGGGCTACGGCAACAGCAGCGCTCAACCCGGTTCTCTACGCTTCTGAGAGAAC 983
Db 1240 ttcaagcgatgcttcagaagattctg 1265
QY 984 TTCAAGCGCTCTCTTCGCCAGCTCTG 1009
```

```
RESULT 5
ID 089222 standard; cDNA; 1618 BP.
AC 089222;
DT 20-OCT-1995 (first entry)
DE Rat mu oploid receptor cDNA.
KW Mu oploid receptor; MOR-1; gene therapy; diagnostic; ss.
OS Rattus sp.
FH key Location/Qualifiers
FT CDS 214..1410
FT /*tag= a
FN W09507983-A.
PD 23-MAR-1995.
PE 13-SEP-1994; U10358.
PR 13-SEP-1993; US-120601.
PA (INDV ) UNIV INDIANA FOUND.
PI Yu L.
DR WPI; 95-131351/17.
DR P-PSDB; R71964.
PT New nucleic acid encoding new human mu oploid receptor - and
PT related vectors, transformed cells, antibodies etc., useful in
PT diagnosis, treatment and drug screening.
PS Disclosure; Page 190-194; 266pp; English.
CC A 365 bp fragment of the mouse delta oploid receptor was used to
CC screen a rat brain cDNA library under low stringency conditions.
CC One positive clone included the sequence given in 089222, encoding a
CC mu oploid receptor, MOR-1 (R71964). MOR-1 was stably expressed in
CC transfect CHO cells.
CC Sequence 1618 BP; 390 A; 486 C; 370 G; 372 T;
SQ
```

```
Query Match 16.1%; Score 365; DB 14; Length 1618;
Best Local Similarity 71.9%; Pred. No. 9,92e-226;
Matches 623; Conservative 0; Mismatches 240; Indels 3; Gaps 2;
Db 403 tccatggtccacagccatcacatcatatgacctctactctatctgtgtgtgtgagctc 462
QY 144 TCCCTCGCCCTTAGCCATCGCATCCCGCGCTCTACTCGCTGTGTGGCATGGGGCTT 203
Db 463 ttccgaacctcgtgtatgtatgtatgtatgaagataaccaaatgaagctccac 522
QY 204 CTGGGCACAGCTCTGTATCTTTGGCATGTCGCCGTACCAAAATTGAAGACCCGCCAC 263
Db 523 aacatctaatcttcaacctgtctcgtgcagagcgcccttagcgacgaatgaactgcctt 582
QY 264 AACATCTACATCTTCAATCTGCTTTGGCTGATGGCTGGCCACAGACGCTGCCCTTC 323
Db 583 cagagtgtcaactaactgatatggaacaatgagcccttcggaaccatctctcgcaagtctg 642
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QY 324 CAGAGCGCCCAAGTACTTGTAGGAAACGTGGCGCTTTGGCGAGCTGTGTCAAGGCTGTG 383
Db 643 atccaatagattactacaacatgttcaccagcatattaccocctcgtcacatgagctg 702
QY 384 CTCTCCATTGACTACTACACATCTTTTACATAGCATCTTCACCCCTACCATCATATAGGCTG 443
Db 703 gaccgtacattgctgtctccaccacgtaaaagoccttgatttcgttacccccgaat 762
QY 444 GACCGCTACATTTGCTGTCTGCATCTGTCAAAAGCCCTGGACTCTCCGAGACACAGCAAG 503
Db 763 gccaaatctgaacgctgtaactgatatctctctctctcgtccatcgtctgacgttaat 822
QY 504 GCCAAGCTGATTAATATATGATGTGGTCTTGCTTCATAGGTGTGGAGTCCCATATAG 563
Db 823 ttcatggcaacacaanaatacagcgaggggtccatagattgacacctacgcttccac 882
QY 564 GTCATGGCAGTGAACCCACCCCGGATGTTGCACTGGATGATGATGTCAGATTCCCAAGT 623
Db 883 ccaacctgtactgtggagaaactgctcaaaatctgttcttactctcgttcatcatg 942
QY 624 CCCAGCTGTGACTGGGACACTGTGACCAAGATCTGCGTGTCTCTTGGCTTGTGCTGTG 683
Db 943 cgcgactcctacatcaactggtgtgttaacgacctgatatgacttaacgaatgaagcttcgc 1002
QY 684 CGGATCCGATCATCAACAGGCTGTGATGAGCTCATGTGACTAGCGGCTGCGGAGGCTGGT 743
Db 1003 atgctatcggctcccaagaagaagaacgaatctgcgcagatcaaccggatggtctg 1062
QY 744 CTGGCTGCTCCGGTTCCAAAGAGAGACCGGACCTGGGCGGACATCGAGCGCATGCTGG 803
Db 1063 gtgtctgtgctgtattatattatgctgtcgtgaccccccatccacatctgaatcataaa 1122
QY 804 GTGGTGGGCGGCTTGCTGTGCTGTGGCGCCATCCATCTCTGATGCTCTGG 863
Db 1123 cgcgtgtatc-acg--attccagaacaacacatttgaacgctttcctggaacttgcatt 1179
QY 864 ACGGTGGTGGACATCAATCGCGGAGACCACTTGGTGGCGGACATCGACCTGGCATTT 923
Db 1180 gctttgggttacacgaacagctgacctgaatccagttcttaccgcttccctggtgaaac 1239
QY 924 GCGCTGGGCTACGGCAACAGCAGCGCTCAACCCGGTTCTCTACGCTTCTGAGAGAAC 983
Db 1240 ttcaagcgatgcttcagaagattctg 1265
QY 984 TTCAAGCGCTCTCTTCGCCAGCTCTG 1009
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```
RESULT 6
ID Q79199 standard; cDNA; 2070 BP.
AC Q79199;
DT 19-APR-1995 (first entry)
DE Rat mu-subtype oploid receptor cDNA.
KW Mu-subtype oploid receptor; MSOR; drug addiction; ds.
OS Rattus rattus.
FH key Location/Qualifiers
FT CDS 83..1154
FT /*tag= a
FT /product= Mu-subtype_oploid_receptor
FN EP-612845-A.
PD 31-AUG-1994.
PE 09-FEB-1994; 101968.
PR 26-FEB-1993; US-026140.
PA (AMCY ) AMERICAN CYANAMID CO.
PI Corbett MJ, Eppeler CM, Shieh H, Zysk JR;
DR WPI; 94-265963/33.
DR P-PSDB; R65188.
PT Pure mu-type oploid receptor protein - and nucleic acid coding
PT for it.
PS Claim 1; Fig 11; 39pp; English.
CC R65188 is the rat mu-subtype oploid receptor protein purified
CC from rat brain membranes, with biotinyl-b-endorphin (R56666)
CC as its ligand. It is encoded by the nucleotide sequence Q79199
```


D	b	1105	gtgttcgttgctcgtattatattgcttgcgtcgtaaccccccatccatctctatgcatcatcaaa	1164
Q	y	804	GTGTGTTGGGGCGCCCTTCGTGGTGTGGTGCGGCATCAACATCTTCGTCATCGCTCGG	863
D	b	1165	gcactgatcaagatcca-gaacacccttcoagac-tgtttccctg- gaactctgacct	1221
Q	y	864	ACGCTGTGGAGCATCATTGCCGCGGACCACCTTGTGGTGGCGGACACGACCTGTGATT	923
D	b	1222	gcctttgggtttcacacaacagctgtctgaaccagttcttttatgcttccctgtatgaaac	1281
Q	y	924	GCGCTGGGACTCGCCCAACAGCACCTCAACCCGGTCTCTCAACGCTTCTCGAGAGAAC	983
D	b	1282	ttoaacgatagttttagagattctg	1307
Q	y	984	TTCAGAGCTCTCTCCGACACTCTG	1009
 RESULT 6 ID O89226 standard; cDNA; 1610 BP.				
AC		O89226;	(first entry)	
DT		20-OCT-1995		
DE		Human mu oploid receptor cDNA.		
KM		Mu oploid receptor; MOR; gene therapy; diagnostic; ss.		
OS		Homo sapiens.		
FH		key	Location/Qualifiers	
FT	CDS	239..1441		
FT	/*tag-	a		
PN		WO507983-A.		
PD		23-MAR-1995.		
PE		13-SEP-1994; U10358.		
PR		13-SEP-1993; US-120601.		
PA		(INDV) UNIV INDIANA FOUND.		
P1		Xu L;		
DR		WPI; 95-131351/17.		
DR		P-PDB: R71966.		
PT		New nucleic acid encoding new human mu oploid receptor - and		
PT		related vectors, transformed cells, antibodies etc., useful in		
PT		diagnosis, treatment and drug screening.		
PS		Claim 5; Page 208-210; 26pp; English.		
CC		A cDNA library constructed from human caudate nucleus mRNA was		
CC		screened with rat mu oploid receptor cDNA under conditions of		
CC		low stringency. One positive clone included the sequence given in		
CC		O89226, encoding a mu oploid receptor MOR (R71966). The cDNA		
CC		is used for prodn. of recombinant MOR, in gene therapy, etc.		
SQ		Sequence 1610 BP; 384 A; 467 C; 359 G; 400 T;		
 Query Match 14.9%; Score 338; DB 14; Length 1610; Best Local Similarity 70.6%; Pred. No. 5,38e-207; Matches 604; Conservative 0; Mismatches 248; Indels 3; Gaps 3				
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Q	y	156	GCCATCGGCATCACCGCGCTCTACTCGGCTGTGGCGCAGTGGGGCTTCTGGCAAGTG	215
D	b	506	cctgtcatcgtatgtgatgttcagatatcccagaatgaagtgtgcacaaacttacatt	565
Q	y	216	CTCGCAGATTGGCATGTGCGGTACCCAAATTGAAGACCGCACCAACATCTTAATC	275
D	b	566	ctcaacctgtcctcygagatgaccttagaccaocagtaaacctgcacctccaagatgtaat	625
Q	y	276	TTCATCTGGGCTTTGGCTGATGCGCTGGCCACACGACGCTGCCCCITCCAAGGGCCAA	335
D	b	626	taacctatggaacatgycacatttignaaccalcctcttccaagatagatgattccatagat	685
Q	y	336	TACTGTAGTGAAGTAGCTGGCCGTTGGCGCAGTGCTGTGTCAGAGGCTGTCTCATTTAC	395
D	b	686	tactataacatgttccacagcatattccacctctgcacacatgatgtgtatcatcaact	745
Q	y	396	TACTCAACAAGTTCACACAGCATCTTCAACCTTCACCAAGATGAAGACGTGGACCGCTAAT	455
D	b	746	gcagctctccaacctcgttaagccttaatttcgtatccgtatcccggaatgaanaattacc	805
Q	y	456	GCTGCTCGCATCCGTATAAACCCCTGSACTTCCGGACACCAAGCCAAAGCCAGCTGATC	515

[illegible]

CC appears to contain a CACACA marker (Q56704) which provides a means
CC to track the inheritance of this gene.
SQ Sequence 829 BP; 182 A; 205 C; 134 G; 214 T;

Query Match 11.7%; Score 266; DB 10; Length 829;
Best Local Similarity 62.8%; Pred. No. 2,91e-157;
Matches 484; Conservative 0; Mismatches 282; Indels 5; Gaps 5;

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Db 18 tacaccaagtgaagaatgacacacatctaatcttcaacctgtctg-cagatgac 76
   |||||
QY 240 TACACCAAAATTGAAGACCGCACCAACATCTACATCTTCATCTGGCTTGATGCG 239
   |||||
Db 77 ttatgccacaagtaccctgccctccagagtgatgaattacttaagggaacatggccatt 136
   |||||
QY 300 CTGGCCACAGAGCAGCTGCCCTTCCAGAGCGCCAGTACTTGAAGAAACGTGGCCGTT 359
   |||||
Db 137 ggaaccatcccttgaagaataatgatactcatagattactatacatggttaccacacata 196
   |||||
QY 360 GAGGAGCTGCTGTGCAAGGCTGTGCTCTCCATGACTTACACACAGTTCACATGACATC 419
   |||||
Db 197 ttacacctctgcacacatgagtggttgatcgatacatctgcagctgcacacctgcaagacc 256
   |||||
QY 420 TTCACCCCTCACCATGATGAGCGGTGACCGCTACATGCTGTGCCATCCTGTCAAGCC 479
   |||||
Db 257 ttatgattccgtactcccnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 316
   |||||
QY 480 CTGGACTTCCGGACACAGCCAGGCCAAGCTGATCATATATGCACTGGGTCTTGGCT 539
   |||||
Db 317 nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 376
   |||||
QY 540 TCAGGTGTGGGGTCCCCATCATGTCATGCGAGTGACCCACCCGGGATGCTGCACTG 589
   |||||
Db 377 gattgtacacttaacattctctcatccaacctggtactgggaaacctgtcgaagatctgt 436
   |||||
QY 600 GATGATGATGCTCCATGCCAGTCCAGCTGCTGACTGGGACACTGTGACCAAGATCTGC 659
   |||||
Db 437 gtttcaatcttgaccttaattatgcagagtgctcatcaattacggtgtgctatggaatgatg 496
   |||||
QY 660 GTGTTCTCTCTTGGCTGCGTGGTGGATCCATCATCAGGCTGTGCTATGGCTCATG 719
   |||||
Db 497 atcttgccctcaagaagtgtccgcatgctctctggtccaaagaagaagacgaatctt 556
   |||||
QY 720 CTACTGCGCCTGGGAGCGCTGCTGCTGCTCCGCTTCCAGGAGAAAGGACCGCAGCCTG 779
   |||||
Db 557 cgaaggataacagaagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 616
   |||||
QY 780 CGGCGCATCAGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 839
   |||||
Db 617 attcaattatgataatcaattaaagccctggttaacaatccca-gaaactagttccagac 675
   |||||
QY 840 ATCCACATCTTCTGTAATGCTGAGAGCTGAGACATCATATGCGCGGACCCACTTGTG 899
   |||||
Db 676 -tgttt-cttggaacttctgcatgtcttaggtttacacaaagcctcctcaaccagtc 733
   |||||
QY 900 GTGGCGGCACTGACACTGTGCAATTTGGCTGGCTAGCCACAGACCTCAACCCGCTT 959
   |||||
Db 734 cttatgcaattctgagataaaactcca-cgatgcttcagagaagtctgt 783
   |||||
QY 960 CTCTAGCCTTCTCTGAGAGAGACTTCAGAGCGCTGCTTCCGCCAGCTCTGT 1010
   |||||
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Search completed: Tue Aug 26 09:53:09 1997
Job time : 286 secs.

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(TM)

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Mparch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Aug 26 07:50:18 1997; MasPar time 14.95 Seconds
Tabular output not generated. 539.070 Million cell updates/sec

Title: >US-08-292-694A-2
Description: (1-380) from US08292694A.pep
Perfect Score: 2839
Sequence: 1 MESPIQLFRGDPGPTCSPSA.....RNTVQDPASMDVGNKRPV 380

Scoring table: PAM 150
Gap 11

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 49.868; Variance 103.252; scale 0.483

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	2839	100.0	380	7	KAPPA-TYPE OPIOID REC	0.00e+00
2	2829	99.6	380	7	KAPPA-TYPE OPIOID REC	0.00e+00
3	2747	96.8	380	7	KAPPA-TYPE OPIOID REC	0.00e+00
4	2610	91.9	380	7	KAPPA-TYPE OPIOID REC	0.00e+00
5	1678	59.1	398	7	KAPPA-TYPE OPIOID REC	0.00e+00
6	1676	59.0	398	7	KAPPA-TYPE OPIOID REC	0.00e+00
7	1675	59.0	400	7	KAPPA-TYPE OPIOID REC	0.00e+00
8	1610	56.7	372	7	KAPPA-TYPE OPIOID REC	0.00e+00
9	1608	56.6	372	7	KAPPA-TYPE OPIOID REC	0.00e+00
10	1597	56.3	372	7	KAPPA-TYPE OPIOID REC	0.00e+00
11	1473	51.9	367	7	KAPPA-TYPE OPIOID REC	0.00e+00
12	1471	51.8	367	7	KAPPA-TYPE OPIOID REC	0.00e+00
13	1465	51.6	370	7	KAPPA-TYPE OPIOID REC	0.00e+00
14	1447	51.0	370	7	KAPPA-TYPE OPIOID REC	0.00e+00
15	980	34.5	391	9	KAPPA-TYPE OPIOID REC	0.00e+00
16	978	34.4	391	9	KAPPA-TYPE OPIOID REC	0.00e+00
17	976	34.4	391	9	KAPPA-TYPE OPIOID REC	0.00e+00
18	968	34.1	388	9	KAPPA-TYPE OPIOID REC	0.00e+00
19	963	33.9	384	9	KAPPA-TYPE OPIOID REC	0.00e+00
20	954	33.6	384	9	KAPPA-TYPE OPIOID REC	0.00e+00
21	938	33.0	368	9	KAPPA-TYPE OPIOID REC	0.00e+00
22	936	33.0	369	9	KAPPA-TYPE OPIOID REC	0.00e+00

23	927	32.7	369	9	SSR2_RAT	SOMATOSTATIN RECEPTOR	1.05e-151
24	922	32.5	369	9	SSR2_MOUSE	SOMATOSTATIN RECEPTOR	1.04e-150
25	912	32.1	369	9	SSR2_HUMAN	SOMATOSTATIN RECEPTOR	1.01e-148
26	850	29.9	333	4	GPR8_HUMAN	PROBABLE G PROTEIN-CO	2.03e-136
27	819	28.8	333	4	SSR3_HUMAN	SOMATOSTATIN RECEPTOR	2.74e-130
28	815	28.7	418	9	SSR3_HUMAN	SOMATOSTATIN RECEPTOR	1.69e-129
29	792	27.9	328	4	GPR7_HUMAN	PROBABLE G PROTEIN-CO	5.83e-125
30	788	27.8	353	9	SSR5_RAT	SOMATOSTATIN RECEPTOR	3.58e-124
31	734	25.9	428	9	SSR3_RAT	SOMATOSTATIN RECEPTOR	1.48e-113
32	732	25.8	428	9	SSR3_MOUSE	SOMATOSTATIN RECEPTOR	5.15e-95
33	639	22.5	359	1	AG2R_CANEA	TYPE-1A ANGIOTENSIN II	4.49e-93
34	629	22.2	359	1	AG2R_HUMAN	TYPE-1A ANGIOTENSIN II	1.71e-92
35	626	22.1	359	1	AG2R_PIG	TYPE-1A ANGIOTENSIN II	1.49e-92
36	623	21.9	355	2	CKR1_HUMAN	C-C CHEMOKINE RECEPTOR	6.53e-92
37	617	21.7	359	1	AG2R_HUMAN	TYPE-1A ANGIOTENSIN II	1.48e-91
38	616	21.7	359	1	AG2R_BOVIN	TYPE-1A ANGIOTENSIN II	1.48e-90
39	615	21.7	359	1	AG2S_RAT	TYPE-1B ANGIOTENSIN I	3.31e-90
40	614	21.6	349	4	GALR_HUMAN	GALANIN RECEPTOR (GAL	3.61e-89
41	610	21.5	359	1	AG2S_MOUSE	TYPE-1B ANGIOTENSIN I	2.14e-89
42	609	21.5	359	1	AG2R_MOUSE	TYPE-1A ANGIOTENSIN I	3.34e-89
43	607	21.4	359	1	AG2R_MELGA	TYPE-1A ANGIOTENSIN II	3.34e-89
44	607	21.4	359	1	AG2R_RAT	TYPE-1A ANGIOTENSIN I	8.15e-89
45	586	20.6	362	1	AG2R_XENLA	TYPE-1-LIKE ANGIOTENS	9.21e-85

ALIGNMENTS

RESULT 1
ID OPRK_MOUSE STANDARD; PRT; 380 AA.

AC P3534;
DI 01-FEB-1994 (REL. 28, CREATED)
DI 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DI 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE KAPPA-TYPE OPIOID RECEPTOR (KOR-1) (MSL-1).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUKARYOTA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE; 93342064.
RA YASUDA K., RAYNOR K., KONG H., BREDER C.D., TAKEDA J., REISINE T.,
RA BELL G.I.;
RL PROC. NATL. ACAD. SCI. U.S.A. 90:6736-6740(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95100967.
RA NISHI M., TAKESHIMA H., MORI M., NAKAGAWARA K.I., TAKEUCHI T.;
RA BIOCHEM. BIOPHYS. RES. COMMUN. 205:1353-1357(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95251663.
RA LIT H.C., LU S., AUGUSTIN L.B., FELSHEIM R.F., CHEN H.C.,
RA LOH H.H., WEI L.N.;
RL BIOCHEM. BIOPHYS. RES. COMMUN. 209:639-647(1995).
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF
AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: BRAIN (NEOCORTEX, HIPPOCAMPUS, AMYGALA,
MEDIAL HYPOTHALAMUS, LOCUS CERULEUS, AND PARABRACHIAL
NUCLEUS).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; L11065; G348249; -;
DR EMBL; D31663; G808876; -;
DR EMBL; D31663; G808876; JOINED.
DR EMBL; D31664; G808876; JOINED.
DR EMBL; S77872; G998532; -;
DR EMBL; S77868; G998532; JOINED.
DR EMBL; S77869; G998532; JOINED.
DR PIR; A48227; A48227.
DR GCRDB; GCR_0635; -;

FT DISULFID 131 210 BY SIMILARITY.
 FT LIPID 345 345 PALMITATE (POTENTIAL).
 FT CARBOHYD 25 25 POTENTIAL.
 FT CARBOHYD 39 39 POTENTIAL.
 FT CONFLICT 42 42 V -> L (IN REF. 2).
 FT CONFLICT 345 345 C -> Y (IN REF. 3).
 SQ SEQUENCE 380 AA; 42668 MW; EBF58A46 CRC32;
 Query Match 99.6%; Score 2829; DB 7; Length 380;
 Best Local Similarity 98.9%; Pred. No. 0.00e+00;
 Matches 376; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Db 1 mespqlfifgepgptcapacallpnsswvfpmwaeedsngvsgedqglepahispalpv 60
 QY 1 MESPLQIFRGDPGPPCSPSACLLPNSSWVFPMWAEEDSNGVSGEDQGLESAHISPALPV 60
 Db 1 itavsvfvgvlgvgnslvmfvitrytkmktatniyifnaladalttmfpgsavy 120
 QY 1 ITAVSVFVVGVLGNSLVMEVITRTKMTAINITIFNLADALTITMFPQSAYL 120
 Db 61 itavsvfvgvlgvgnslvmfvitrytkmktatniyifnaladalttmfpgsavy 120
 QY 61 ITAVSVFVVGVLGNSLVMEVITRTKMTAINITIFNLADALTITMFPQSAYL 120
 Db 121 mswpfgdvlgkivisidyymfifcltmvsvdrylavchpvykaldfrtphkakiini 180
 QY 121 MNSWFGDVLCKIVISIDYYNMFISIFCLTMVSVDRYLAUCHPVKALDFRTPHAKIINI 180
 Db 181 ctwllassvgisatvlggtkyredvdiectsqfddesvwdlfnkicvtfafavpvl 240
 QY 181 CWTLLASSVGISATVLGGTKYREDVDIECSLQFPDDEYSWMDLFMKICVEFAFVAVPVL 240
 Db 191 ctwllassvgisatvlggtkyredvdiectsqfddesvwdlfnkicvtfafavpvl 240
 QY 191 CWTLLASSVGISATVLGGTKYREDVDIECSLQFPDDEYSWMDLFMKICVEFAFVAVPVL 240
 Db 241 itvgytlmrlfklsvrllsgsrekdnrlrtiklylvvavfllcwprhifllvealg 300
 QY 241 IITVGYTLMRLKSVRLLSGRKDNRLRTIKLYLVVAVFLLCWPRHIFLLVEALG 300
 Db 241 itvgytlmrlfklsvrllsgsrekdnrlrtiklylvvavfllcwprhifllvealg 300
 QY 241 IITVGYTLMRLKSVRLLSGRKDNRLRTIKLYLVVAVFLLCWPRHIFLLVEALG 300
 Db 301 stshstaissyfciagynslpnylfafldenfkrcfdcfplkmtmergstary 360
 QY 301 STSHSTAISYFCIAGYNSLNPYLFALDENFKRCRFDCEFPKMERGSTARY 360
 Db 361 rntvgdpasmtidvggmknkv 380
 QY 361 RNTVODPASMDVGGMKNKV 380
 RESULT 3 STANDARD; PRT; 380 AA.
 AC P41145;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DE 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE KAPPA-TYPE OPIOID RECEPTOR (KOR-1).
 GN OPRK1 OR OPRK.
 OS HOMO SAPIENS (HUMAN).
 OC EUDAKOTA; METAFOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 NC 11
 RC SEQUENCE FROM N.A.
 RP TISSUE=PLACENTA.
 RX MEDLINE; 9438360.
 RA MAUSSON E., BARE L.A., YANG D.;
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 202:1431-1437(1994).
 RM 12
 SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA.
 RX MEDLINE; 95350200.
 RA STIMONIN F., GAVRIANUS-RUFF C., BEFORT K., LANNES B., MICHELETTI G.,
 RA MATTEL M.-G., CHARON G., BLOCH B., KIEFFER B.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 92:7006-7010(1995).
 RM 13
 SEQUENCE FROM N.A.
 RC TISSUE=BRAIN.
 RX MEDLINE; 95174504.
 RA ZHU J., CHEN C., XUE J.C., KUNAPUDI S., DERIEL J.K., LIU-CHEN L.-Y.;
 RL LIFE SCI. 56:201-207(1995).
 CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
 ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR

CC FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF
 CC AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; U11053; G532060; -;
 DR EMBL; U17298; G596070; -;
 DR EMBL; L37362; G722618; -;
 DR PIR; J02338; J02338.
 DR MIM; 165196; -;
 DR PROSITE; PS00237; G-PROTEIN_RECEPTOR.
 KM G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
 KM PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
 FT DOKAIN 1 58
 FT TRANSSEM 59 85
 FT DOKAIN 86 95
 FT TRANSSEM 96 117
 FT DOKAIN 118 132
 FT TRANSSEM 133 154
 FT DOKAIN 155 173
 FT TRANSSEM 174 196
 FT DOKAIN 197 222
 FT TRANSSEM 223 247
 FT DOKAIN 248 275
 FT TRANSSEM 276 299
 FT DOKAIN 300 311
 FT TRANSSEM 312 333
 FT DOKAIN 334 380
 FT DISULFID 131 210
 FT LIPID 345 345
 FT CARBOHYD 25 25
 FT CARBOHYD 39 39
 FT CONFLICT 2 2
 SQ SEQUENCE 380 AA; 42659 MW; 1980629E CRC32;
 Query Match 96.8%; Score 2747; DB 7; Length 380;
 Best Local Similarity 93.9%; Pred. No. 0.00e+00;
 Matches 357; Conservative 17; Mismatches 6; Indels 0; Gaps 0;
 Db 1 mespqlfifgepgptcapacallpnsswvfpmwaeedsngvsgedqglepahispalpv 60
 QY 1 MESPLQIFRGDPGPPCSPSACLLPNSSWVFPMWAEEDSNGVSGEDQGLESAHISPALPV 60
 Db 61 itavsvfvgvlgvgnslvmfvitrytkmktatniyifnaladalttmfpgsavy 120
 QY 61 ITAVSVFVVGVLGNSLVMEVITRTKMTAINITIFNLADALTITMFPQSAYL 120
 Db 121 mswpfgdvlgkivisidyymfifcltmvsvdrylavchpvykaldfrtphkakiini 180
 QY 121 MNSWFGDVLCKIVISIDYYNMFISIFCLTMVSVDRYLAUCHPVKALDFRTPHAKIINI 180
 Db 181 ctwllassvgisatvlggtkyredvdiectsqfddesvwdlfnkicvtfafavpvl 240
 QY 181 CWTLLASSVGISATVLGGTKYREDVDIECSLQFPDDEYSWMDLFMKICVEFAFVAVPVL 240
 Db 241 itvgytlmrlfklsvrllsgsrekdnrlrtiklylvvavfllcwprhifllvealg 300
 QY 241 IITVGYTLMRLKSVRLLSGRKDNRLRTIKLYLVVAVFLLCWPRHIFLLVEALG 300
 Db 301 stshstaissyfciagynslpnylfafldenfkrcfdcfplkmtmergstary 360
 QY 301 STSHSTAISYFCIAGYNSLNPYLFALDENFKRCRFDCEFPKMERGSTARY 360
 Db 361 rntvgdpasmtidvggmknkv 380
 QY 361 RNTVODPASMDVGGMKNKV 380
 RESULT 4 STANDARD; PRT; 380 AA.
 AC P41144;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)


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Db 188 nvcnwllssaiglpwmfnatlkkyrg-s-idctltfshptw-ywenllkicvffaifmp 244
QY 179 NCIWMLASSVGSISALVIGTKVREDVDVIECSLOPDEYSWMDLEKICVFVFAVIP 238
Db 245 vlltvcyglmlrlkksvmlsgskednrlrltmtvlyvavafivcwpdihlyvika 304
QY 239 VLIITVCYTLMLRLKSVRLSGSKEDNRLRLTKVLVYVAVAFIICWPIHIFIVEA 298
Db 305 llttpectfcvswbfclalgytncslpnylafaIdenfkrcfrefcldptsstlegqna 364
QY 289 LGSTSHSTAALSSYFCIALGYTNSLNPVLAFLDENFKRCFDFCPDKRMEROSTN 358
Db 365 ttrgtrephstanty 380
QY 359 RVR-NTVODPASMEDV 373

RESULT 6
ID OPRM_RAT STANDARD; PRT; 398 AA.
AC P35357;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DE MU-TYPE OPIOID RECEPTOR (MOR-1) (OPIOID RECEPTOR B) (MOR1).
GN MOR-B.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN:
RX MEDLINE; 93351652.
RA FUKUDA K., KATO S., MORI K., NISHI M., TAKESHIWA H.;
RL FEBS LETT. 327:311-314(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN:
RX MEDLINE; 94052137.
RA WANG J.-B., IMAI Y., EPLER M.C., GREGOR P., SPIVAK C., UHL G.R.;
RL PROC. NATL. ACAD. SCI. U.S.A. 90:10230-10234(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN:
RX MEDLINE; 93341493.
RA CHEN Y., MESTER A., LIU J., HURLEY J.A., YU L.;
RL MOL. PHARMACOL. 44:8-12(1993).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN:
RA BUNZOW J.R., GRANDY D.K., KELLY M.;
RL SUBMITTED (SEP-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-OLFACTORY BULB;
RX MEDLINE; 94059560.
RA THOMPSON R.C., MANSOUR A., AKIL H., WATSON S.J.;
RL NEURON 11:903-913(1993).
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
FOR BETA-ENDOPHEIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: BRAIN, WITH HIGH CONCENTRATIONS IN THE
BRAINSTEM AND CEREBRUM, NOT DETECTED IN CEREBELLUM.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; D16349; G391867; -
DR EMBL; L20684; G409150; -
DR EMBL; L13069; G348351; -
DR EMBL; U02083; G403574; -
DR EMBL; L22455; G437672; -
DR PIR; S34593; S34593.
DR GCRDB; GCR_0633; -
DR GCRDB; GCR_0637; -

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DR GCRDB; GCR_0639; -
DR GCRDB; GCR_0640; -
DR GCRDB; GCR_0644; -
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR.
KM G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
NM PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 64
FT TRANSMEM 65 94
FT DOMAIN 95 103
FT TRANSMEM 104 121
FT DOMAIN 122 143
FT TRANSMEM 144 163
FT DOMAIN 164 193
FT TRANSMEM 194 209
FT DOMAIN 210 234
FT TRANSMEM 235 257
FT DOMAIN 258 280
FT TRANSMEM 281 303
FT DOMAIN 304 311
FT TRANSMEM 312 328
FT DOMAIN 329 398
FT DISULFID 140 217
FT LIPID 351 351
FT CARBOHYD 9 9
FT CARBOHYD 31 31
FT CARBOHYD 38 38
FT CARBOHYD 46 46
FT CARBOHYD 53 53
FT CONFLICT 245 245
SQ SEQUENCE 398 AA; 44494 MM; 2021013D CRC32;

Query Match 59.0%; Score 1676; DB 7; Length 398;
Best Local Similarity 66.1%; Pred. No. 7,01e-303;
Matches 209; Conservative 53; Mismatches 50; Indels 4; Gaps 4;

Db 68 altmalysivcvgvlgfnflmyvlyrytkmktatniylnlajadalsclpfgsvn 127
QY 59 PVILTAAYSVFVGVGLVNSLMVEFVIRYTKMKATNTIYFNALADLVTTTFMEQNAV 118
Db 128 ylmgwpggtllkklvlsldygmftsfclctsvdyivcphvkaldtrpnakiv 187
QY 119 YLMSWPGGDVLCIKIVISIDIDYNNFTSIFTLTMSVDRYIVCHVKALDTRTPKAKII 178
Db 188 nvcnwllssaiglpwmfnatlkkyrg-s-idctltfshptw-ywenllkicvffaifmp 244
QY 179 NCIWMLASSVGSISALVIGTKVREDVDVIECSLOPDEYSWMDLEKICVFVFAVIP 238
Db 245 vlltvcyglmlrlkksvmlsgskednrlrltmtvlyvavafivcwpdihlyvika 304
QY 239 VLIITVCYTLMLRLKSVRLSGSKEDNRLRLTKVLVYVAVAFIICWPIHIFIVEA 298
Db 305 llttpectfcvswbfclalgytncslpnylafaIdenfkrcfrefcldptsstlegqna 364
QY 289 LGSTSHSTAALSSYFCIALGYTNSLNPVLAFLDENFKRCFDFCPDKRMEROSTN 358
Db 365 ttrgtrephstanty 380
QY 359 RVR-NTVODPASMEDV 373

RESULT 7
ID OPRM_HUMAN STANDARD; PRT; 400 AA.
AC P35372;
DT 01-JUN-1994 (REL. 29, CREATED)
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE MU-TYPE OPIOID RECEPTOR (MOR-1).
GN OPRM1 OR MOR1.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE-BRAIN;
RX MEDLINE; 94139928.
RA WANG J.-B., JOHNSON P.S., PERSICO A.M., HAWKINS A.L., GRIFFIN C.A.,
RA UHL G.R.;
RL FEBS LETT. 338:217-222(1994).
RN [12]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA MESTER A. JR., HURLEY J.H., BYE L.S., CAMPBELL A., TIAN M.,
RA CHEN Y., YU L.;
RL SUBMITTED (XXX-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
CC FOR BETA-ENDORPHIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; L25119; G452073; -.
DR GCRDB; L29301; G459832; -.
DR GCRDB; GCR_0985; -.
DR GCRDB; GCR_0966; -.
DR MIM; 600018; -.
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR.
RW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 56 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 67 96 1 (POTENTIAL).
FT DOMAIN 97 105 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 106 123 2 (POTENTIAL).
FT DOMAIN 124 145 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 146 165 3 (POTENTIAL).
FT DOMAIN 166 195 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 196 211 4 (POTENTIAL).
FT DOMAIN 212 236 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 237 259 5 (POTENTIAL).
FT DOMAIN 260 282 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 283 305 6 (POTENTIAL).
FT DOMAIN 306 313 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 314 330 7 (POTENTIAL).
FT DOMAIN 331 400 CYTOPLASMIC (POTENTIAL).
FT DISULFID 142 219 BY SIMILARITY.
FT LIPID 353 353 PALMITATE (POTENTIAL).
FT CARBOHYD 9 9 POTENTIAL.
FT CARBOHYD 12 12 POTENTIAL.
FT CARBOHYD 33 33 POTENTIAL.
FT CARBOHYD 40 40 POTENTIAL.
FT CARBOHYD 48 48 POTENTIAL.
FT CONFLICT 51 51 N -> D (IN REF. 2).
FT CONFLICT 234 234 V -> L (IN REF. 2).
SQ SEQUENCE 400 AA; 44764 MW; 3F40D610 CRC32;

Query Match 59.0%; Score 1675; DB 7; Length 400;
Best Local Similarity 66.6%; Pred. No. 1,12e-302;
Matches 207; Conservative 52; Mismatches 49; Indels 3; Gaps 3;

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DB 367 rirgntcdhps 377
QY 359 RVRNTVDDPAS 369

RESULT 8 STANDARD; PRT; 372 AA.
ID ORPD_RAT
AC P33533;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE DELTA-TYPE OPIOID RECEPTOR (DOR-1) (OPIOID RECEPTOR A).
GN ROR-A.
OS RATTUS NORVEGICUS (RAT).
OC EURAROTIA; METAFOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE; 93351652.
RA FUKUDA K., KATO S., MORI K., NISHI M., TAKESHIMA H.;
RL FEBS LETT. 327:311-314(1993).
RN [12]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
RX MEDLINE; 94322412.
RA ABOOD M.E., NOEL M.A., FARNSWORTH J.S., TAO Q.;
RL J. NEUROSCI. RES. 37:714-719(1994).
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. HIGHLY
CC STEREOSPECIFIC. RECEPTOR FOR ENKEPHALINS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; D16348; G391865; -.
DR EMBL; U00475; G514211; -.
DR PIR; S34592; S34592.
DR GCRDB; GCR_0638; -.
DR GCRDB; GCR_0805; -.
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR.
RW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 45 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 46 75 1 (POTENTIAL).
FT DOMAIN 76 84 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 85 102 2 (POTENTIAL).
FT DOMAIN 103 124 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 125 144 3 (POTENTIAL).
FT DOMAIN 145 174 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 175 190 4 (POTENTIAL).
FT DOMAIN 191 215 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 216 238 5 (POTENTIAL).
FT DOMAIN 239 261 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 262 284 6 (POTENTIAL).
FT DOMAIN 285 293 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 294 310 7 (POTENTIAL).
FT DOMAIN 311 372 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 18 18 POTENTIAL.
FT CARBOHYD 33 33 POTENTIAL.
FT CARBOHYD 121 198 BY SIMILARITY.
FT LIPID 333 333 PALMITATE (POTENTIAL).
SQ SEQUENCE 372 AA; 40449 MW; 59F5E850 CRC32;

Query Match 56.7%; Score 1610; DB 7; Length 372;
Best Local Similarity 65.6%; Pred. No. 1.94e-289;
Matches 214; Conservative 55; Mismatches 48; Indels 9; Gaps 7;

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QY      82 FYIIRYTKKTAINTYFNIALADALVYTTMPQSAVILMNSWPGDVLCIKVISIDYNN 141
Db      132 mftsifltlmsvdyriavchpvcakldfrtpakakliniciwlasgvygvpimnavtqp 191
QY      142 MFTSIFLTLMMSVDRIYAVCHPVCALDFRTPAKAKLINICIMWLASSGISATVIGTKV 201
Db      192 rdga-vv-cmlgfesp--swywdvtckicvflfafrvpdllitvcyglmlllsrvlls 247
QY      202 RDVDVVICSLQFPDDEXSW-WDLFMKICVFYFAVIVPILIIYVCTLMILRLKSVRLIS 260
Db      248 gskekdrslrirtlmvnyvgafrvcwcapihlfvlywtlvdtdrtdplvvaalhlciailg 307
QY      261 GSREKDRMLRRTIKTLVLYVAVFIICWPIHFIILVEALGISTSHSTA-ALSSYFCIALG 319
Db      308 yansslnpvlyafldenfkrcfrlgc 333
QY      320 YTNSSLNPVLYAFLDENFKRCFRDRC 345

RESULT 9
ID      OPND_HUMAN      STANDARD:      PRT;      372 AA.
AC      P41143;
DT      01-FEB-1995 (REL. 31, CREATED)
DI      01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DI      01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE      DELTA-TYPE OPTOID RECEPTOR (DOR-1).
GN      OPBD1 OR OPBD.
OS      HOMO SAPIENS (HUMAN).
OC      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN      EUHERIA; PRIMATES.
[1]
RP      SEQUENCE FROM N.A.
RC      TISSUE-CEREBRAL CORTEX, AND STRIATUM;
RX      MEDLINE; 94260835.
RA      KNAPP R.J., MALATYNSKA E., FANG L., LI X., BABIN E., NGUYEN M.,
RA      SANTORO G., VARGA E.V., HRUBY V.J., ROESKE W.R., YAMAMURA H.I.;
RL      LIFE SCI. 54:463-469(1994).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE; 95107267.
RA      SIMONIN F., BEFORT K., GAVERIAUX-RUPE C., MATHEES H., NAPPET V.,
RA      LANNES B., MICHELETTI G., KIEFFER B.;
RL      MOL. PHARMACOL. 46:1015-1021(1994).
CC      -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC      ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. HIGHLY
CC      STEREOSELECTIVE. RECEPTOR FOR ENKEPHALINS.
CC      -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR      EMBL; U07882; G497314; -.
DR      EMBL; U10504; E162517; -.
DR      MIM; 165195; -.
DR      PROSITE; PS00237; G-PROTEIN-RECEPTOR.
RW      G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW      PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT      DOMAIN 1 45
FT      TRANSSEM 46 75
FT      DOMAIN 76 84
FT      TRANSSEM 85 102
FT      DOMAIN 103 124
FT      TRANSSEM 125 144
FT      DOMAIN 145 174
FT      TRANSSEM 175 190
FT      DOMAIN 191 215
FT      TRANSSEM 216 238
FT      DOMAIN 239 261
FT      TRANSSEM 262 284
FT      DOMAIN 285 293
FT      TRANSSEM 294 310
FT      DOMAIN 311 372
FT      CARBOHYD 18
FT      CARBOHYD 33
FT      DISULFID 121
FT      LIPID 333

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FT      CONFLICT 27 27 F -> C (IN REF. 2).
FT      CONFLICT 40 41 PG -> AR (IN REF. 2).
FT      CONFLICT 348 348 P -> A (IN REF. 2).
FT      CONFLICT 370 370 R -> A (IN REF. 2).
SQ      SEQUENCE 372 AA; 40450 MW; CFF92985 CRC32;

Query Match
Best Local Similarity 56.6%; Score 1608; DB 7; Length 372;
Matches 213; Conservative 56; Mismatches 48; Indels 9; Gaps 8;

Db      15 lfansdays-a-fpsaganaaspppgssas-sialataialysavoaagllnavlm 71
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Db      72 fgivrytkmktatniyifnialadaltstjpfgsakylmewpbgelckavlsidynn 131
QY      82 FYIIRYTKKTAINTYFNIALADALVYTTMPQSAVILMNSWPGDVLCIKVISIDYNN 141
Db      132 mftsifltlmsvdyriavchpvcakldfrtpakakliniciwlasgvygvpimnavtqp 191
QY      142 MFTSIFLTLMMSVDRIYAVCHPVCALDFRTPAKAKLINICIMWLASSGISATVIGTKV 201
Db      192 rdga-vv-cmlgfesp--swywdvtckicvflfafrvpdllitvcyglmlllsrvlls 247
QY      202 RDVDVVICSLQFPDDEXSW-WDLFMKICVFYFAVIVPILIIYVCTLMILRLKSVRLIS 260
Db      248 gskekdrslrirtlmvnyvgafrvcwcapihlfvlywtlvdtdrtdplvvaalhlciailg 307
QY      261 GSREKDRMLRRTIKTLVLYVAVFIICWPIHFIILVEALGISTSHSTA-ALSSYFCIALG 319
Db      308 yansslnpvlyafldenfkrcfrlgc 333
QY      320 YTNSSLNPVLYAFLDENFKRCFRDRC 345

RESULT 10
ID      OPND_MOUSE      STANDARD:      PRT;      372 AA.
AC      P32300;
DT      01-OCT-1993 (REL. 27, CREATED)
DI      01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
DI      01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE      DELTA-TYPE OPTOID RECEPTOR (DOR-1) (K56) (MSL-2).
OS      MUS MUSCULUS (MOUSE).
OC      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN      EUHERIA; RODENTIA.
[1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE; 93101664.
RA      KIEFFER B.L., BEFORT K., GAVERIAUX-RUPE C., HIRTH C.G.;
RL      PROC. NATL. ACAD. SCI. U.S.A. 89:12048-12052(1992).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE; 93110361.
RA      EVANS C.U., KEITH D.E. JR., MORRISON H., MAGENDZO K., EDWARDS R.H.;
RL      SCIENCE 258:1952-1955(1992).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      TISSUE-BRAIN.
RX      MEDLINE; 93342064.
RA      YASUDA K., RAYNOR K., KONG H., BREDER C.D., TAKEDA J., REISINE T.,
RA      BELL G.L.;
RL      PROC. NATL. ACAD. SCI. U.S.A. 90:6736-6740(1993).
RN      [4]
RP      SEQUENCE FROM N.A.
RA      KEITH D.E. JR., ANTON B., EVANS C.U.;
RL      PROC. WEST. PHARMACOL. SOC. 36:299-306(1993).
RN      [5]
RP      SEQUENCE OF 8-372 FROM N.A.
RX      MEDLINE; 94022364.
RA      BZDEGA T., CHIN H., KIM K., JUNG H.H., KOZAK C.A., KLEE W.A.;
RL      PROC. NATL. ACAD. SCI. U.S.A. 90:9305-9309(1993).
RN      [6]
RP      3D-STRUCTURE MODELLING.

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RX MEDLINE; 97001837.
RA ALKORIN I., LOEW G.H.;
RL PROTEIN ENG. 9:573-583(1996).
CC -1- FUNCTION: INHIBITS NEUTROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. HIGHLY
CC SEROPROTECTIVE. RECEPTOR FOR ENKEPHALINS
CC -1- TISSUE SPECIFICITY: BRAIN. WITH HIGH CONCENTRATIONS IN THE BASAL
CC GANGLIA AND LIMBIC REGIONS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
DR EMBL; L06322; G192943; -.
DR EMBL; L07271; -. NOT ANNOTATED_CDS.
DR EMBL; L11064; G348247; -.
DR EMBL; S65335; G442326; -.
DR EMBL; S66181; G435782; -.
DR PIR; S37807; S37807.
DR PIR; H48227; B48227.
DR GCRDB; GCR_0229; -.
DR GCRDB; GCR_0493; -.
DR GCRDB; GCR_0634; -.
DR GCRDB; GCR_0842; -.
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 45 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 46 75 1 (POTENTIAL).
FT DOMAIN 76 84 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 85 102 2 (POTENTIAL).
FT DOMAIN 103 124 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 125 144 3 (POTENTIAL).
FT DOMAIN 145 174 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 175 190 4 (POTENTIAL).
FT DOMAIN 191 215 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 216 238 5 (POTENTIAL).
FT DOMAIN 239 261 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 262 284 6 (POTENTIAL).
FT DOMAIN 285 293 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 294 310 7 (POTENTIAL).
FT DOMAIN 311 372 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 18 18 POTENTIAL.
FT CARBOHYD 33 33 POTENTIAL.
FT DISULFID 121 198 BY SIMILARITY.
FT LIPID 333 333 PALMITATE (POTENTIAL).
SQ SEQUENCE 372 AA; 40561 MW; 514022F5 CRC32;
Query Match 56.3%; Score 1597; DB 7; Length 372;
Best Local Similarity 66.7%; Pred. No. 8.56e-287;
Matches 206; Conservative 51; Mismatches 46; Indels 6; Gaps 5;

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RESULT 11
ID ORF_RAT STANDARD; PRT; 367 AA.
AC P35370;
DE 01-JUN-1994 (REL. 29, CREATED)
DE 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DE 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE PROBABLE OPIOID RECEPTOR (ROR-C) (XOR1).
OS EIKAROTA; METAZO; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=BRAIN;
RX MEDLINE; 94215703.
RA FUKUDA K., KATO S., MORI K., NISHI M., TAKESHIMA H., IWABE N.,
RA MIYATA T., HOUTANI T., SUGIMOTO T.;
RL FEBS LETT. 343:42-46(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=HIPPOCAMPUS;
RA MENG F., XIE G., ALFRED M., THOMPSON R., HOVERSTEN M., WATSON S.,
RA AKIL H.;
RL SUBMITTED (JAN-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX MEDLINE; 94307401.
RA BUNZOW J.R., SAEZ C., MORTRU D., BOUVIER C., WILLIAMS J.T., LOW M.,
RA GRANDY D.K.;
RL FEBS LETT. 347:284-288(1994).
RN [4]
RP SEQUENCE FROM N.A.
RC MEDLINE; 94307400.
RA CHEN Y., FAN Y., LIU J., MESTEK A., TIAN M., KOZAK C.A., YU L.;
RL FEBS LETT. 347:279-283(1994).
RN [5]
RP SEQUENCE FROM N.A.
RC MEDLINE; 95096849.
RA LACHOWICZ J.E., SHEN Y., MONGMA F.J., SIBLEY D.R.;
RL J. NEUROCHEM. 64:34-40(1995).
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE; 94298959.
RA WANG J.B., JOHNSON P.S., IMAI Y., PERSICO A.M., OZEMBERGER B.A.,
RA EPLER C.M., UHL G.R.;
RL FEBS LETT. 348:75-79(1994).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX MEDLINE; 95182817.
RA WICK M.J., MINNERATH S.R., LIN X., ELDE R.P., LAW P.Y., LOH H.H.;
RL BRAIN RES. MOL. BRAIN RES. 27:37-44(1994).
CC -1- FUNCTION: OPIOID RECEPTOR WITH A POTENTIAL ROLE IN MODULATING A
CC NUMBER OF BRAIN FUNCTIONS, INCLUDING INSTINCTIVE BEHAVIOURS AND
CC EMOTIONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS
CC WHICH INHIBITS ADENYLYL CYCLASE.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN SEVERAL BRAIN AREAS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; D1638; G533395; -.
DR EMBL; U05239; G451844; -.
DR EMBL; U01913; G487965; -.
DR EMBL; L28144; G496220; -.
DR EMBL; U07871; G606803; -.
DR EMBL; L33916; G557200; -.
DR EMBL; L29419; G510719; -.
DR PIR; S46238; S46238.
DR PIR; S43655; S43655.
DR GCRDB; GCR_0834; -.
DR GCRDB; GCR_0898; -.

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DR GCRDB; GCR_0912; -
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 47
FT TRANSSEM 48 74
FT DOMAIN 75 84
FT TRANSSEM 85 106
FT DOMAIN 107 121
FT TRANSSEM 122 143
FT DOMAIN 144 162
FT TRANSSEM 163 185
FT DOMAIN 186 208
FT TRANSSEM 209 233
FT DOMAIN 234 261
FT TRANSSEM 262 285
FT DOMAIN 286 297
FT TRANSSEM 298 319
FT DOMAIN 320 365
FT DISULFID 120 197
FT LIPID 331 331
FT CARBOHYD 21 21
FT CARBOHYD 26 26
FT CARBOHYD 36 36
FT CONFLICT 105 105
FT CONFLICT 226 226
FT CONFLICT 246 246
FT CONFLICT 348 348
SQ SEQUENCE 367 AA; 40523 MW; 7FD40CCC CRC32;

Query Match 51.9%; Score 1473; DB 7; Length 367;
Best Local Similarity 59.38; Pred. No. 1.36e-261;
Matches 188; Conservative 63; Mismatches 61; Indels 5; Gaps 5;

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100 tlpfgtdlllgfwpfgnaloktviaidymftstflamsvdyvaalchpirladvr 159
111 lmpfosavylmmswprgvdvckrtvisidymftstflamsvdyvaalchpirladvr 170
160 tsckagavvaalasalasvgyvgyvgyvgyvgyvgyvgyvgyvgyvgyvgyvgy 215
171 tlpkaktinlclwllasvgsaisavlggkvrdvdielcslofppd-deyswmdlfnkic 229
216 lflsfllpylllsvcslnlrrlgvllsgsrkrdrolrltlrlyvvaavfygcmtp 275
230 vefvafvlpilittvcttllmlrkvrlslsgsrkrdrolrltlrlyvvaavfygcmtp 289
276 vgyfvavglvgvpgsetavallrftcalgyvncinpllyafidenfkacfkfcoass 335
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350 mrmrqslnvrvntvod 366

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RA YASUDA K., JONES E., REISINE T., BELL G.I.;
RL SUBMITTED (JAN-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95100967.
RA NISHI M., TAKEISHIMA H., MORI M., NAKAGAWARA K.I., TAKEUCHI T.;
RL BIOCHEM. BIOPHYS. RES. COMMUN. 205:1353-1357(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC SPRAIN-SPRAGUE-DANLEY; TISSUE-BRAIN;
RA MATTHEWS H.W.D.; TO EMBL/GENBANK/DBJ DATA BANKS.
RL SUBMITTED (SEP-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [4]
RP SEQUENCE OF 1-357 FROM N.A.
RC SPRAIN-BALB/C; TISSUE-SPLEEN;
RA HALFORD W.P., GEBARDT B.W., CARR D.J.J.;
RL SUBMITTED (AUG-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: OPIOID RECEPTOR WITH A POTENTIAL ROLE IN MODULATING A
CC NUMBER OF BRAIN FUNCTIONS, INCLUDING INSTINCTIVE BEHAVIOURS AND
CC EMOTIONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS
CC WHICH INHIBITS ADENYLYL CYCLASE.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; U04952; G440880; -.
DR EMBL; D31667; G808874; -.
DR EMBL; D31666; G808874; JOINED.
DR EMBL; X91813; G1008982; -.
DR EMBL; U14165; G540093; -.
DR GCRDB; GCR_0891; -.
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 47
FT TRANSSEM 48 74
FT DOMAIN 75 84
FT TRANSSEM 85 106
FT DOMAIN 107 121
FT TRANSSEM 122 143
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FT TRANSSEM 298 319
FT DOMAIN 320 365
FT DISULFID 120 197
FT LIPID 331 331
FT CARBOHYD 21 21
FT CARBOHYD 26 26
FT CARBOHYD 36 36
FT CONFLICT 105 105
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SQ SEQUENCE 367 AA; 40523 MW; 7FD40CCC CRC32;

REFERENCE
1 (bases 1 to 3081)
AUTHORS
Yousoufian H., McAfee M. and Kwiatkowski D.J.
TITLE
Cloning and chromosomal localization of the human cytoskeletal
alpha-actinin gene reveals linkage to the beta-spectrin gene
JOURNAL
Am. J. Hum. Genet. 47 (1), 62-71 (1990)
MEDLINE
90274024
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APPLICANT: FALLA, Cristina
APPLICANT: TOMEL, Lidia
TITLE OF INVENTION: METHOD FOR REPRODUCING IN VITRO THE
TITLE OF INVENTION: PROTEOLYTIC ACTIVITY OF THE NS3 HEPATITIS C VIRUS (HCV)
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEWMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,356
FILING DATE: 23-AUG-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: DE FRANCESCO-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 631 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-700-356-1
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11

Sequence 2, Application US/08700356
GENERAL INFORMATION:
APPLICANT: DE FRANCESCO, Raffaele
APPLICANT: FALLA, Cristina
APPLICANT: TOMEL, Lidia
TITLE OF INVENTION: METHOD FOR REPRODUCING IN VITRO THE
TITLE OF INVENTION: PROTEOLYTIC ACTIVITY OF THE NS3 HEPATITIS C VIRUS (HCV)
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEWMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,356
FILING DATE: 23-AUG-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: DE FRANCESCO-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-700-356-2
STWTVVGVLAALAAVCLITGSVVIWRIIISGRPAIVPDBRELLYQEFDEMEEC1

; Sequence 3, Application US/08700356
; GENERAL INFORMATION:
; APPLICANT: DE FRANCESCO, Raffaele
; APPLICANT: FALLA, Cristina
; APPLICANT: TOWEL, Lidia
; TITLE OF INVENTION: METHOD FOR REPRODUCING IN VITRO THE
; TITLE OF INVENTION: PROTEOLYTIC ACTIVITY OF THE NS3 HEPATITIS C VIRUS (HCV)
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEWMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,356
; FILING DATE: 23-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: DE FRANCESCO-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
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; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: /note="Xaa at position 34 means
; OTHER INFORMATION: Abu (2-Aminobutyric acid)"
US-08-700-356-3
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CC were used in the isolation of the NS2-NS4 regions of the Hepatitis C
CC Virus (HCV) gene of the invention (see also R29660, R29559-60 and
CC R29843-51). These RNA sequences were isolated from the serum of a
CC patient suffering from hepatitis C (HC). The isolated RNA sequences
CC were converted into cDNA using transcriptase in the presence of one
CC of the primer sequences given in Q32578-79. The sequences were then
CC amplified using primer pairs. The cDNA sequences isolated represent
CC different alleles of the same region of the HCV


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QY 121 MNSWPFQDVCLCKIVISIDYINMFTSIFLTMMASVDRIYAVCHPYKALDFRPIKAKIINI 180
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QY 301 STSHSTAALSYFCIALGYTNSSLNPLYAFIDENKRCFRDCFPPIKMRMERGSTURY 360
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QY 361 RNTVQDPASMRDVGGMKNKV 380

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RESULT 2

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ID R7678; standard; Protein; 380 AA.
AC R7678;
DE 11-DEC-1995 (first entry)
DE Rat kappa opiate receptor.
KW Kappa opiate receptor; mu opiate receptor; hMOR; opiate agonist;
OS opiate antagonist; drug abuse; analgesic.
KW Rattus sp.
FN W09520667-A1.
PD 03-AUG-1995.
PE 30-JAN-1995; 001144.
PR 28-JAN-1994; US-188275.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (USSH ) US SEC DEPT HEALTH.
PA Johnson PS, Persico AM, Uhl G, Wang J;
PI WPI; 95-275452/36.
PT New DNA encoding human mu opiate receptor - used esp. for screening
PT cpls. for activity as opiate agonists or antagonists
PS Disclosure: Page 29-30; 49pp; English.
CC hMOR cDNA was obt'd. from a human cerebral cortical cDNA library
CC screened with fragments of a rat mu opiate receptor. The encoded
CC protein showed homology to rat mu, delta and kappa opiate
CC receptors (R76781-83).
SQ Sequence 380 AA;

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Query Match 99.6%; Score 2829; DB 14; Length 380;

Best Local Similarity 98.9%; Pred. No. 1.55e-259; Mismatches 1; Indels 0; Gaps 0;

Matches 376; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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QY 301 STSHSTAALSYFCIALGYTNSSLNPLYAFIDENKRCFRDCFPPIKMRMERGSTURY 360
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RESULT 3

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ID R72591 standard; Protein; 380 AA.
AC R72591;
DE 01-DEC-1995 (first entry)
DE Mammalian kappa opiod receptor protein.
KW Mammalian kappa opiod receptor; mouse delta opiod receptor; analgesic;
KW amplification; primer; rat; probe; E.coli; R1-PCR; hypnotic compound; ds.
OS Rattus rattus.
FH key Location/Qualifiers
FT CDS 111..1253
FT /tag= a
FT /product= kappa opiod receptor
FN J07070191-A.
PD 14-MAR-1995.
PE 30-JUL-1993; 190261.
PR 09-JUL-1993; JP-170591.
PA (TAKE ) TAKEDA CHEM IND LTD.
DR WPI; 95-144857/19.
DR N-PSDB; Q86725.
PT kappa opiod receptor protein and cells expressing it - useful
PT for the screening of compounds for analgesic and hypnotic
PT properties
PS Claim 2; Page 9-10; 15pp; Japanese.
CC The amino acid sequence of the novel mammalian kappa opiod receptor.
CC The gene was isolated by amplifying a fragment from rat brain mRNA by
CC reverse transcriptase-PCR (R1-PCR) using primers Q86726-7 derived from
CC the mouse delta-opiod receptor gene. This fragment was cloned into the
CC plasmid pCRIT to produce pR1. The plasmid pR1 was used to probe a rat
CC brain DNA library in lambda ZAPII to obtain a clone of the rat kappa
CC opiod receptor gene, designated pKOPR2. This clone was introduced into
CC E.coli JM109 for production of the receptor protein. The receptor protein
CC is useful for screening of analgesic and hypnotic compounds including
CC peptides and proteins.
SQ Sequence 380 AA;

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Query Match 99.4%; Score 2823; DB 14; Length 380;

Best Local Similarity 98.7%; Pred. No. 5.98e-259; Mismatches 1; Indels 0; Gaps 0;

Matches 375; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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QY 241 IITVCYTLMLIRKLSVRLISGSRKDNRLRRITKLVYVAVFIIICWTPIHIFILVEALG 300

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Db 301 stshstavisyyfcialgytnsslnpvlafldenfkrcfdcfpikmmersgturv 360
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Db 361 rntvqdpasmrdvggmknkpv 380
QY 361 RNTVQDPASMRDVGGMKNKPV 380

RESULT 4
ID R88722 standard; Protein: 380 AA.
AC R88722;
DE 04-SEP-1996 (first entry)
DI Human kappa opioid receptor.
KW Human; kappa opioid receptor; psychiatric disorder; cardiovascular;
OS neurology; diagnosis.
PN Homo sapiens.
PD 25-JAN-1996.
PE 07-JUL-1995; F00912.
PF 11-JUL-1994; FR-008531.
PI (UYST-) UNIV PASTEUR STRASBOURG LOUIS.
PI Kletter B, Simonin F;
DR WPI; 96-097628/10.
DR N-PSDB; t12550.
PT New nucleic acid encoding the human Kappa opioid receptor - useful
PT in diagnosis and therapy, and for isolating receptor ligands and
PT modulators
PS Claim 7; Page 13-15; 30pp; French.
CC The sequence coding for the human kappa opioid receptor was
CC obtained from two overlapping cDNA fragments isolated from a
CC human placental cDNA library. The fragments were amplified from
CC the library using PCR primers based on the sequence of human
CC genomic clones which hybridised with a murine delta receptor cDNA
CC probe. Nucleotide probes derived from the kappa delta receptor
CC coding sequence are useful for diagnosis of neurological, cardio-
CC vascular and psychiatric disorders associated with opioid
CC receptors. The receptor can be used for identifying e.g. agonists
CC of its activity for potential use as analgesics.
SQ Sequence 380 AA;

Query Match 96.7%; Score 2746; DB 17; Length 380;
Best Local Similarity 93.7%; Pred. No. 2, 01e-25;
Matches 356; Conservative 18; Mismatches 6; Indels 0; Gaps 0;

Db 1 ndspigifirgepyptcacsacilpnssawfpywaeqdsngsedaglepahispaipy 60
QY 1 MESPIQIRGDPGPRCSPSACILPNSSWEPNMAESDNGSGVSDQQLSESHIPALPY 60
Db 61 lltaysvrvfvglyvgnslvmfvllrrtkmtatniyifnlaladalvtttmpfgstvy 120
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Db 121 mnswpfvgvackiyisidymfscifellmmsvdyriavchpkaaldftrplakakini 180
QY 121 MNSWPFVGVACKIYISIDYMFSCIFELLMMSVDRIAVCHPKAALDFTRPLAKAKINI 180
Db 121 mnswpfvgvackiyisidymfscifellmmsvdyriavchpkaaldftrplakakini 180
QY 121 MNSWPFVGVACKIYISIDYMFSCIFELLMMSVDRIAVCHPKAALDFTRPLAKAKINI 180
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QY 241 lltayvtlmilrlksvrlslsgrkdnrlrrtlltlyrvavfvcvtpihifllvealg 300
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QY 301 STSHSTALSSYYFCIALGYTNSSLNPLVLAFLDENFKRCFDFCPIMKMEROSTNRV 360
Db 361 rntvqdpaylridgmknkpv 380
QY 361 RNTVQDPASMRDVGGMKNKPV 380

```

```

RESULT 5
ID R67672 standard; Protein: 295 AA.
AC R67672;
DE 18-AUG-1995 (first entry)
DI Human kappa opioid receptor partial protein.
KW Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;
KW transmembrane domain; somatostatin; receptor; human; expression vector;
KW truncate; chimaeric; assay; probe.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Misc-difference 169
FT /label= Any amino acid
FT Misc-difference 181
FT /label= Any amino acid
FT Misc-difference 265
FT /label= Any amino acid
FT Misc-difference 269
FT /label= Any amino acid
PN W09428132-A.
PD 08-DEC-1994.
PE 20-MAY-1994; U05747.
PF 30-MAY-1993; US-066296.
PR 30-JUL-1993; US-100694.
PR 05-NOV-1993; US-147592.
PI (ARCH-) ARCH DEV CORP.
PI Bell GI, Reisine T, Yasuda K;
DR WPI; 95-022804/03.
DR N-PSDB; Q75931.
PT Polynucleotides and peptides derived from opioid receptor
PT polypeptides - for use in therapeutic compositions and in
PT screening assays for useful drug substances.
PS Claim 12; Page 236-239; 300pp; English.
CC The partial amino acid sequence of the novel human kappa opioid receptor.
CC The corresponding gene was isolated from a human brain hippocampus cDNA
CC library using a probe from the mouse kappa opioid receptor gene (Q75926).
CC The gene is missing the N-terminal sequence. The C-terminal sequence is
CC very similar to the mouse kappa opioid receptor sequence. Of the
CC C-terminal 293 amino acids, 281 residues are identical and 6 residues
CC have conservative substitutions. The gene encoding the human opioid
CC receptor can be placed in a suitable expression vector for production of
CC the protein in a cell. The opioid receptors thus produced are useful for
CC the development of novel assays designed to select or improve substances,
CC capable of interacting with the opioid receptor proteins, for use in
CC diagnosis, drug design and therapeutic applications.
SQ Sequence 295 AA;

Query Match 75.0%; Score 2130; DB 12; Length 295;
Best Local Similarity 92.5%; Pred. No. 2, 57e-191;
Matches 273; Conservative 13; Mismatches 8; Indels 1; Gaps 1;

Db 1 ytkmktatniyifnlaladalvtttmpfgstvy lmswpfvgvackiyisidymfscif 60
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QY 61 fllmmsvdyriavchpkaaldftrplakakini ciavlssvgsaisavlggtkredv 120
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Db 207 viēcslqfpddqyswmdlfmkicvfa fvpvl lltayvtlmilrlksvrlslsgrk 266
QY 207 viēcslqfpddqyswmdlfmkicvfa fvpvl lltayvtlmilrlksvrlslsgrk 266
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QY 181 xnlrrtlltlyrvavfvcvtpihifllvealgstshstavisyyfcialgytnssln 240
Db 267 rntvqdpaylridgmknkpv 295
QY 267 RNTVQDPASMRDVGGMKNKPV 295
Db 241 pilyalldenfkrcfdcfpikmmersgturv rntvqdpaylridgmknkpv 295
QY 241 PLYALFDENFKRCFDFCPIMKMEROSTNRV RNTVQDPASMRDVGGMKNKPV 295

```


PT New DNA encoding human mu opiate receptor - used esp. for screening
 PS cpgs. for activity as opiate agonists or antagonists
 FT Disclosure: Page 26-28; 49pp; English.
 CC hMOR cDNA was obt. from a human cerebral cortical cDNA library
 CC screened with fragments of a rat mu opiate receptor. The encoded
 CC protein showed homology to rat mu, delta and kappa opiate
 CC receptors (R76781-83).
 CC Sequence 398 AA;

Query Match	59.0%;	Score 1676;	DB 14;	Length 398;
Best Local Similarity	66.1%;	Pred. No. 3.57e-147;		
Matches	209;	Conservative	53;	Mismatches 50.

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QY      59 pvtitayivsvfvgigvgnslmefvlrrtymkmtatnnyifnaladalavtttmfösaav 118
```

D5 128 ylnqtwpfllcklvisidymnfsifllctmsvdviavchpvkaldfrtrpnakiv 187
 ||| :||| :||||| ||||| ||||| ||||| ||||| :||| :
 QY 119 ylnmswpegdvlcklvisidymnfsifllctmsvdrviavchpvkaldfrtrpnakii 178

```
D3      188 nvnwnllssaiglpymfmattkkyrgq-s-ldctltfsaptw-ywenllkicvifafimp 244  
       |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|  
QY     179 NCIWMLSSVGSIAIVLGKTKVREVDYIESIOEPDDEYSMDI.FMTCVFEVAAEVTP 238
```

[illegible]

```
D0      305 lltipettlqtwshñcialgyltynslpnvlyafldenfkrcrfcicptsttiegqnst 364
       | : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
D1      309 TCSHSHGAAIACGVVQCTTICITWVETVYKVVNLT 368
```

```

Db      365  rrrqntrephstantv 380
      ||| || : |:: |
      ||| || : |:: |

```

RESULT 9

DE Rat mu opioid receptor.
DI 20-Oct-1995 (first entry)
AC R71964;
AD n/1304 standard; protein; 398 AA.

KW mu opioid receptor; MOR-1; gene therapy; diagnostic.
 OS Rattus sp.
 PN W09507983-A.
 ID 23-Mar-1995

PF 13-SEP-1994; U10358.
PR 13-SEP-1993; US-120601.
PA (INDV) UNIV INDIANA FOUND.
I

DR WPI: 95-131351/17.
DR N-PSDB: Q89222.
PT New nucleic acid encoding new human mu opioid receptor - and

CC A 365 bp fragment of the mouse delta oviduct receptor was used to

CC screen at rat brain cDNA library under low stringency conditions.
CC One positive clone included the sequence given in Q89222, encoding a
CC mu opioid receptor, MOR-1 (R71964). MOR-1 was stably expressed in
CC transfected CHO cells.

Seq Sequence 398 AA;
Query Match 59.0%; Score 1674; DB 13; Length 398;

68	altimalysivcvgqlfionflvmyvirytkmkrtatnjlfnlajadaafstlfnaswn	137
Matches	208; Conservative	54; Mismatches
		Indels
		Gaps

```

QY      59  PVIITAVSYVEVGLVGNLSLVFVILIRYTKMKATNIXIFNLALDALVTITMPQSAV 118
      128  Ylmtwfpqfclcklvisidvymfstsift]ctmsvdvjavchouka]dettwvsk:: 167

```

```

QY      119 YLNNSPEDVJCKIVISIDYYNMTSFTLTNMSVRYIKVCHPRALPFRRLKAKII 178
      188 nvcnwjlssaqlpymfmatekyrys-s-ldctltfshpvt-yuenllkicvffialmp 244
QY      179 NCIIMLLASVSISIAIVJAGTRVEDDVIVIECSLQFPDEXSWMDLPMKICVFEFAVIP 238

```

QY 239 VLIIVCYTLMIRKSVRLSSGSEKEDNRLRRTKVLVAVAVFIICWTPHIFELVEA 298

QY 299 LGSTSHSTAALSYFICALGYINSLNVLPAEDENEFRCFBCFPIKRMENQSTN 358

QY 359 RVR-NTVQDPASMRDV 373

	RESULT	10
ID	R76780	standard; Protein; 400 AA.
AC	R76780;	

DE Human mu opiate receptor.
KW Mu opiate receptor; hMOR; opiate agonist; opiate antagonist; drug abuse; analgesic.

CS	homu saplans.	Location/Qualifiers
FH	Key	
FT	Modified_site	9
FT	/label=Glycosylation	

```

F1 /note="N-linked glycosylation site"
ET Modified_site 11
ET /label= Glycosylation
ET /note="N-linked glycosylation site"

```

```
FT Modified_site 32
FT /label=glycosylation
FT /note="N-linked glycosylation site"
```

FT	/label= Glycosylation
FT	/note= "N-linked glycosylation site"
FT	Modified_site 48

```

.. /label= glycosylation
FT /note= "N-linked glycosylation"
FT
FT Domain 68..87
FT /label= Transmembrane domain

```

ET	Domain	107..125
ET	/label=	Transmembrane_domain
ET	Domain	144..165
ET	/label=	Transmembrane_domain

FT	Domain	188..208
FT	/label=	Transmembrane_domain
FT	Domain	236..256
FT	/label=	Transmembrane_domain

FT	Domain	284..304
FT	/label=	Transmembrane_domain
FT	Domain	322..341

11	/lawet - klausenmemorand_euclid
PN	W09520667-A1.
PD	03-AUG-1995.
PF	30-JAN-1995: W01144.

PK 28-JAN-1994; US-188275.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (USSH) US SEC DEPT HEALTH.
PI Johnson BS Persio M th) C West T

DR WPI; 95-275452/36.
DR N-PSDB; Q93102.
PT New DNA encoding human mu opiate receptor - used esp. for screening

claim 1; Page 25-26; 49pp; English.
hMOR cDNA was obt'd. from a human cerebral cortical cDNA library
screened with fragments of a rat mu opiate receptor. Expression

CC opiate specific ligand. Recombinant hMOR1 can be used to screen
CC compounds for analgesic activity.

Sequence 400 AA;

Query Match 59.0%; Score 1675; DB 14; Length 400;

Best Local Similarity 66.6%; Pred. No. 4,47e-147;
Matches 207; Conservative 52; Mismatches 49; Indels 3; Gaps 3;

```

Db      70  ailmajysivcvgvlgfnfvmvvyrvtkmkatniyifnladalatslpfgsvn 129
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      59  FVITAYSVFVGVGLVNSLVVFVIRYTKMKATNIYIFNLADALVTTMPQSAV 118
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      130 ylmgtwpgftlclktivlsidyymftsiflctmsvdrtylavchpypkaldrtrmkli 189
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      119 YKMSWPEFDVLCIKIVISIDYNNFTSIFTLTKMSVDXYIAVCHPVKALDRTPKAKII 178
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      190 rvcawmlssaiglvmfmatkkyrg-s-ldctltfshptv-ywenlykicvffafam 246
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      179 NICTWMLASSVGSAIYVIGTKVREDVDVIECSIQFDPDEKSWMDLFKICVFAFAVIR 238
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      247 vllttvcyglmllrlksvrmjsgskednrlrlrltmvlyvvavfivcwrphlyvika 306
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      239 VLIITVCTYLMILRLKSVRLSSGREKDRNLRITKVLVAVVAFIICWPIHIFIIVEA 298
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      307 lvtlpettfcvswbfclalytncslhnpvlyafldenfkrcfiefcjpstnsieqmnt 366
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      299 IGSYSHSTALSSYFCIALGYTNSLNPVLYAFIDENFKCFRDFCFPIKMREROSTN 358
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      367 rlrntrrhps 377
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      359 RYRNTVQDPAS 369
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

RESULT 12
ID R67670 standard; Protein; 372 AA.

```

AC R67670;
DE 11-DEC-1995 (first entry)
DE Rat delta opiate receptor.
KW Delta opiate receptor; mu opiate receptor; hMOR; opiate agonist;
KW opiate antagonist; drug abuse; analgesic.
OS Rattus sp.
PN W09520667-A1.
PF 03-AUG-1995;
PF 30-JAN-1995; U01144.
PR 28-JAN-1994; US-188275.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (USSH ) US SEC DEPT HEALTH.
PI Johnson PS, Persico AM, Uhl G, Wang J;
PI WPI: 95-275452/36.
DR New DNA encoding human mu opiate receptor - used esp. for screening
PT cDNAs for activity as opiate agonists or antagonists
PS Disclousure; Page 28-29; 49pp; English.
CC hMOR cDNA was obt'd. from a human cerebral cortical cDNA library
CC screened with fragments of a rat mu opiate receptor. The encoded
CC protein showed homology to rat mu, delta and kappa opiate
CC receptors (R676781-83).
SQ Sequence 372 AA;

```

Query Match 56.7%; Score 1610; DB 14; Length 372;

Best Local Similarity 65.6%; Pred. No. 9.01e-141;
Matches 214; Conservative 55; Mismatches 48; Indels 9; Gaps 7;

```

Db      15  liaavsdltfpaasanaagsgpar--sas-salalaialaiaavavllgnvym 71
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      22 LIPNSWSPPPNAESDSNGSEDOQLSAHISPAIPYIITAYSVFVGVGLVNSLVW 81
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      72  fctivrtklktatnlyifnladalatslpfgskayvmewpfcclckavlsldyn 131
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      82  FVIRTRTKKATNIYIFNLADALVTTMPQSAVYKMSWPEFDVLCIKIVISIDYIN 141
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      132 mftsfcltmmavdrylavchpypkaldrftfpakaklinicwlaagvvpimwmatqp 191
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      142 MFTSTLTLMASVDRIYAVCHPVKALDRFTPLAKAKINICIMWLASVGSIAIVLGTV 201
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

```

Db      192 rda-vv-cltqfisp--swywdtvckicvflafayvpyllivcvglmllrlsvrlls 247
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      202 REVVDVIECSIQFDPDEKSW-WDLFKICVFAFAVIFVLIITVCTYLMILRLKSVRLS 260
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      248 gskedslrlrltmvlyvvagafvcwaphlfiyvlwlvdrpdrplyvvaalhlciaig 307
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      261 GSRKDRNLRITKVLVAVVAFIICWPIHIFILVDAISTSHSTK-ALESSYFCIALG 319
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      308 yanslrvlyafldenfkrcfqlc 333
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      320 YTNSSLNPVLYAFIDENFKCFRDFC 345
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

RESULT 12
ID R67670 standard; Protein; 372 AA.

```

AC R67670;
DE 17-AUG-1995 (first entry)
DE Mouse delta opioid receptor MOR1.
KW Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;
KW transmembrane domain; somatostatin; receptor; human; expression vector;
KW truncate; chimaeric; assay; probe.
OS Mus musculus.
PN W09428132-A.
PF 08-DEC-1994.
PF 20-MAY-1994; U05747.
PR 20-MAY-1993; US-066296.
PR 30-JUL-1993; US-100694.
PR 05-NOV-1993; US-147592.
PA (ARCH-) ARCH DEV CORP.
PI Bell GI, Retsine T, Yasuda K;
PI WPI: 95-022804/03.
DR N-PESD: 075927.
PT Polynucleotides and peptides derived from opioid receptor
PT polypeptides - for use in therapeutic compositions and in
PT screening assays for useful drug substances.
PS Claim 5; Page 215-221; 300pp; English.
CC The amino acid sequence of the novel mouse delta opioid receptor MOR1.
CC The corresponding gene was isolated from a mouse brain cDNA library using
CC a fragment (amplified from the cDNA library with primers 075929-30) as a
CC probe. The primers are based on the conserved sequences present in the
CC second and third transmembrane domains of somatostatin (SRI) receptor
CC subtypes STR1, STR2 and STR3. The 1.3 kb Bcor1-Saci fragment from the
CC mouse delta opioid receptor clone, lambda msl-2, was subcloned into the
CC CMV promoter-based expression vector pCMV-6c. The resultant construct
CC pCMV-msl-2 was transfected into COS-1 cells for protein production. The
CC gene encoding the opioid receptor can be used to produce complete,
CC truncated or chimaeric opioid receptor proteins. The opioid receptors
CC thus produced are useful for the development of novel assays designed to
CC select or improve substances, capable of interacting with the opioid
CC receptor proteins, for use in diagnosis, drug design and therapeutic
CC applications.
SQ Sequence 372 AA;

```

Query Match 56.3%; Score 1597; DB 13; Length 372;

Best Local Similarity 66.7%; Pred. No. 1.64e-139;
Matches 206; Conservative 51; Mismatches 46; Indels 6; Gaps 5;

```

Db      47  alalaialysavcavglgnavlmfgivrytklktatniyifnladalatslpfgs 106
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      57 AIPVITAYSVFVGVGLVNSLVVFVIRYTKMKATNIYIFNLADALVTTMPQOS 116
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      107 akylmetwpgfclckavlsidyymftsifltnmsvdrtylavchpypkaldrfpakak 166
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      117 AYVLMNSWPEFDVLCIKIVISIDYNNFTSIFTLTKMSVDXYIAVCHPVKALDRTPKAK 176
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      167 lnicwvlasgvgvplmmavtqprda-vv-cmlqfisp--swywdtvckicvflaf 222
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      177 INICWMLASSVGSAIYVIGTKVREDVDVIECSIQFDPDEKSW-WDLFKICVFAFAV 235
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      223 vvpillivcvglmllrlsvrllsgskedslrlrltmvlyvvagafvcwaphlfi 282
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      236 VIPVLIITVCTYLMILRLKSVRLSSGREKDRNLRITKVLVAVVAFIICWPIHIFIL 295
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

Db 283 wvliydinrrdpjlvaaahlciaalyanslpvlyafidenfkrcfrqjctpcgrqep 342
 QY 296 VEAAGSTSHSTA-ALSSYFFCALGTNSLNPAFLIDENFKRCFRDCEPKRMER 354
 Db 343 gslirprga 351
 QY 355 QSTNRYRNT 363

RESULT 13

ID R48629 standard; Protein; 372 AA.
 AC R48629;
 DI 15-SEP-1994 (first entry)
 DE Sequence of murine delta opioid receptor deduced from the
 DE DOR-1 cDNA clone.
 KM Opioid receptor; morphine; opiate.
 OS Mus musculus.
 FH Key
 FH Region Location/Qualifiers
 FT /label= putative membrane spanning region
 FT Region 85..102
 FT /label= see above
 FT Region 125..144
 FT /label= see above
 FT Region 168..189
 FT /label= see above
 FT Region 215..238
 FT /label= see above
 FT Region 262..284
 FT /label= see above
 FT Region 295..308
 FT /label= see above
 PN M09404552-A.
 PD 03-MAR-1994;
 PF 13-AUG-1993; 007665.
 PR 13-AUG-1992; US-929200.
 PA (REGC) UNIV CALIFORNIA.
 PI Edwards RE, Evans CJ, Kaufman D, Keith DE;
 DR WPI: 94-083099/10.
 DR N-PSDB: Q56700.
 FT DNA encoding opioid receptors and antibodies against this
 FT receptor - used to express and locate these receptors, and screen
 FT cpts. for opioid (anti)agonist activity
 PS Claim 10; Fig 5; 74pp; English.
 CC A cDNA library was constructed using mRNA isolated from the NG109-15
 CC cell line. A single clone, named the DOR-1 clone was isolated.
 CC Comparisons with known sequences in Genbank showed highest homology
 CC between DOR-1 and the G-protein-coupled somatostatin receptor. Other
 CC features of the DOR-1 clone AA sequence deduced from the cDNA
 CC sequence include 3 consensus glycosylation sites at residues 18 and
 CC 33 (predicted to be in the extracellular N-terminal domain), and at
 CC residue 310 (close to the C-terminus and predicted to be
 CC intracellular). Phosphokinase C consensus sites are present within
 CC predicted intracellular domains, at residues 242/255/344 & 352.
 CC Seven putative membrane-spanning regions were identified. The DOR-1
 CC clone produces a delta receptor with a predicted mol. wt. of 40,558
 CC katoms prior to post-translational modifications.
 SQ Sequence 372 AA;

Query Match 56.3%; Score 1597; DB 9; Length 372;
 Best Local Similarity 66.7%; Pred. No. 1,64e-139;

Matches 206; Conservative 51; Mismatches 46; Indels 6; Gaps 5;

Db 47 alalaiaalyaavcavglignvymfgivrytkiktatniyifnaladalaatstipfqs 106
 QY 57 ALPIIIIVSVVWVVGGLVNSLVFVIRTKMTATNIYIFNALADALVTTMPRQS 116
 Db 107 akylmetwfpfgellckavlsidyymfstsftltmmsvdyriavchpykalditpapak 166
 QY 117 AVYLMNSWPFEDVLCIKIVISIDYINMFSTITLTMMSVDRIIAVCHPYKALDFRPLAK 176
 Db 167 linciwlaasgvvplmvmavtrpdrga-vv-cmlgtfsgp--swywdtvtkicvflfaf 222

QY 177 IINICIMWLASSVGSISALVIGSTKVRVEDVIECSIQEPDDEXSW-WDLENKICVFEAF 235
 Db 223 vvpiliiitvcyglmllrlsvrllsgskedrsirritmvlvvgafvccaphilivi 282
 QY 236 VIPVLIIVCYITLIRKSVRLSSGREKDRNLRIKVLVVAVAFICWTPIHIFILV 295
 Db 283 wvliydinrrdpjlvaaahlciaalyanslpvlyafidenfkrcfrqjctpcgrqep 342
 QY 296 VEAAGSTSHSTA-ALSSYFFCALGTNSLNPAFLIDENFKRCFRDCEPKRMER 354
 Db 343 gslirprga 351
 QY 355 QSTNRYRNT 363

RESULT 14

ID R66503 standard; Protein; 371 AA.
 AC R66503;
 DI 19-JAN-1995 (first entry)
 DE Murine delta opioid receptor.
 KM Delta opioid; enkephalin; receptor; mouse; murine; analgesic; pain;
 KM drug addiction; neurological disorder; psychiatric; disorder;
 KM cardiovascular disorder.
 OS Mus musculus.
 PN FR2697850-A.
 PD 13-MAY-1994.
 PF 10-NOV-1992; 013526.
 PR 10-NOV-1992; FR-013526.
 PA (UYST-) UNIV PASTEUR STRASBOURG LOUIS.
 PI Kieffer B;
 DR WPI: 94-178255/22.
 DR N-PSDB: Q66556.
 FT New nucleic acid encoding opioid receptor - and related
 FT polypeptide, antisense nucleic acid, probes, recombinant cells
 FT and ligands, useful in diagnosis and treatment of e.g.
 FT neurological disorders
 PS Claim 8; Page 19-20; 29pp; French.
 CC A cDNA bank constructed from hybridoma NG108-15, was used to
 CC transfect COS-1 cells. The cells were tested for ability to bind
 CC tritium-labelled Tyr-D-Phe-Gly-Phe-Leu-Thr, in the presence or
 CC absence of the opioid antagonist naloxone. Clone K56 was isolated
 CC from a positive colony and found to contain a 2216bp insert. This
 CC cDNA encodes a delta opioid (enkephalin) receptor with apparent
 CC dissociation constant 1.4nM and Bmax 3.9-6.4 pmole/mg protein.
 SQ Sequence 371 AA;

Query Match 52.8%; Score 1499; DB 10; Length 371;
 Best Local Similarity 64.9%; Pred. No. 5.12e-130;
 Matches 200; Conservative 52; Mismatches 51; Indels 5; Gaps 5;

Db 47 alalaiaalyaavcavglignvymfgivrytkiktatniyifnaladalaatstipfqs 106
 QY 57 ALPIIIIVSVVWVVGGLVNSLVFVIRTKMTATNIYIFNALADALVTTMPRQS 116
 Db 107 akylmetwfpfgellckavlsidyymfstsftltmmsvdyriavchpykalditpapak 166
 QY 117 AVYLMNSWPFEDVLCIKIVISIDYINMFSTITLTMMSVDRIIAVCHPYKALDFRPLAK 176
 Db 167 linciwlaasgvvplmvmavtr-pgmwgyacs-sspv-qlv1-dtvcikcvcflfafv 222
 QY 177 IINICIMWLASSVGSISALVIGSTKVRVEDVIECSIQEPDDEXSWWMDLENKICVFEAFV 236
 Db 223 vvpiliiitvcyglmllrlsvrllsgskedrsirritmvlvvgafvccaphilivi 282
 QY 237 IPVLIIVCYITLIRKSVRLSSGREKDRNLRIKVLVVAVAFICWTPIHIFILV 296
 Db 283 wvliydinrrdpjlvaaahlciaalyanslpvlyafidenfkrcfrqjctpcgrqep 342
 QY 297 VEAAGSTSHSTA-ALSSYFFCALGTNSLNPAFLIDENFKRCFRDCEPKRMERQ 355
 Db 343 gslirprga 350


```

Db      61  lltavsvvfvvglvgnslvmfvlirytckmktatniyifnlaladaltvttmpfgsavy 120
      |||
QY      61  lltavsvvfvvglvgnslvmfvlirytckmktatniyifnlaladaltvttmpfgsavy 120
Db      121 mmswfgdvclckivlsldyymftsifltlmsvdyavchpvcakldfrtpjaklilnl 180
      |||
QY      121 mmswfgdvclckivlsldyymftsifltlmsvdyavchpvcakldfrtpjaklilnl 180
      |||
QY      121 mmswfgdvclckivlsldyymftsifltlmsvdyavchpvcakldfrtpjaklilnl 180
      |||
Db      181 clwllasvgsaisvlgctkcvredvavieoslqfpddeswvdlfmkicvfaaviy 240
      |||
QY      181 clwllasvgsaisvlgctkcvredvavieoslqfpddeswvdlfmkicvfaaviy 240
      |||
Db      241 lltvgytlmlrlksvrlisgsrekdnrlrrtkllyvvavfllcwtpihfilvealg 300
      |||
QY      241 lltvgytlmlrlksvrlisgsrekdnrlrrtkllyvvavfllcwtpihfilvealg 300
      |||
Db      301 sthsavlsyfficalgytnslnpvlyafidenfkrcfcpikmmersgtnry 360
      |||
QY      301 sthsavlsyfficalgytnslnpvlyafidenfkrcfcpikmmersgtnry 360
      |||
Db      361 rntvgdpsamrdvgmknpy 380
      |||
QY      361 rntvgdpsamrdvgmknpy 380
      |||

RESULT 2
ENTRY   S36143 #type complete
TITLE   kappa opioid receptor - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE    10-Dec-1993 #sequence_revision 19-Oct-1995 #text_change
        06-Sep-1996
ACCESSIONS S36143; S38825; S36102; S39015; A48789
REFERENCE
#authors Nishi, M.; Takeshima, H.; Fukuda, K.; Kato, S.; Mori, K.
#journal FEBS Lett. (1993) 330:77-80
#title    cDNA cloning and pharmacological characterization of an
          opioid receptor with high affinities for
          kappa-subtype-selective ligands.
#accession S36143
#status preliminary
#molecule_type mRNA
#residues 1-380 #label NIS

REFERENCE
#authors Chen, Y.; Mestek, A.; Liu, J.; Yu, L.
#journal Biochem. J. (1993) 295:625-628
#title    Molecular cloning of a rat kappa opioid receptor reveals
          sequence similarities to the mu and delta opioid receptors.
#accession S38825
#status preliminary
#molecule_type mRNA
#residues 1-380 #label CHE
#cross-references GB:L2201

REFERENCE
#authors Minami, M.; Toya, T.; Katao, Y.; Maekawa, K.; Nakamura, S.;
#journal Onogi, T.; Kaneko, S.; Seton, M.
#journal FEBS Lett. (1993) 329:291-295
#title    Cloning and expression of a cDNA for the rat kappa-opioid
          receptor.
#accession S36102
#status preliminary
#molecule_type mRNA
#residues 1-41, 'V', 43-380 #label MIN

REFERENCE
#authors Li, S.; Zhu, J.; Chen, C.; Chen, Y.W.; Deriel, J.R.; Ashby,
#journal B.; Liu-Chen, L.Y.
#journal Biochem. J. (1993) 295:629-633
#title    Molecular cloning and expression of a rat kappa opioid
          receptor.
#accession S39015
#molecule_type mRNA
#residues 1-344, 'Y', 346-380 #label LIS

REFERENCE
#authors Meng, F.; Xie, G.

```

```

#Journal Proc. Natl. Acad. Sci. U.S.A. (1993) 90:9954-9958
#Title Cloning and pharmacological characterization of a rat kappa
#cross-references MJDID:94052210
#accession A48789
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-380 #label RES
#cross-references EMBL:U00442; NID:9403486; CDS_PID:9403487
SUMMARY #length 380 #molecular_weight 42688 #checksum 9972

Query Match 99.6%; Score 2829; DB 14; Length 380;
Best Local Similarity 98.9%; Pred. No. 0.00e+00;
Matches 376; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db      1  mespigifrgdpptcpsacilpnsswfpwmaesdsrgsvgsedqqlapahispay 60
      |||
QY      1  mespigifrgdpptcpsacilpnsswfpwmaesdsrgsvgsedqqlapahispay 60
      |||
Db      61  lltavsvvfvvglvgnslvmfvlirytckmktatniyifnlaladaltvttmpfgsavy 120
      |||
QY      61  lltavsvvfvvglvgnslvmfvlirytckmktatniyifnlaladaltvttmpfgsavy 120
      |||
Db      121 mmswfgdvclckivlsldyymftsifltlmsvdyavchpvcakldfrtpjaklilnl 180
      |||
QY      121 mmswfgdvclckivlsldyymftsifltlmsvdyavchpvcakldfrtpjaklilnl 180
      |||
Db      181 clwllasvgsaisvlgctkcvredvavieoslqfpddeswvdlfmkicvfaaviy 240
      |||
QY      181 clwllasvgsaisvlgctkcvredvavieoslqfpddeswvdlfmkicvfaaviy 240
      |||
Db      241 lltvgytlmlrlksvrlisgsrekdnrlrrtkllyvvavfllcwtpihfilvealg 300
      |||
QY      241 lltvgytlmlrlksvrlisgsrekdnrlrrtkllyvvavfllcwtpihfilvealg 300
      |||
Db      301 sthsavlsyfficalgytnslnpvlyafidenfkrcfcpikmmersgtnry 360
      |||
QY      301 sthsavlsyfficalgytnslnpvlyafidenfkrcfcpikmmersgtnry 360
      |||
Db      361 rntvgdpsamrdvgmknpy 380
      |||
QY      361 rntvgdpsamrdvgmknpy 380
      |||

RESULT 3
ENTRY   JC2434 #type complete
TITLE   kappa-opioid receptor - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE    21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change
        05-Apr-1995
ACCESSIONS JC2434
REFERENCE
#authors Nishi, M.; Takeshima, H.; Mori, K.; Nakagawara, K.; Takeuchi,
#journal T.
#journal Biochem. Biophys. Res. Commun. (1994) 205:1353-1357
#title    Structure and chromosomal mapping of genes for the mouse
          kappa-opioid receptor and an opioid receptor homologue
          (MOR-C).
#accession JC2434
#status preliminary
#molecule_type mRNA
#residues 1-380 #label NIS
#cross-references DDBJ:D31663

GENETICS #map_position 1A2-3
          #introns 86/2; 204/1
KEYWORDS receptor
SUMMARY #length 380 #molecular_weight 42630 #checksum 9705

Query Match 99.2%; Score 2816; DB 14; Length 380;
Best Local Similarity 99.5%; Pred. No. 0.00e+00;
Matches 378; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db      1  mespigifrgdpptcpsacilpnsswfpwmaesdsrgsvgsedqqlapahispay 60

```

```

QY 1 MESPLOIFRGDGPFCPSACILPNSSSWFPMAESDSNGSGSEDOQLESASHIPALPV 60
Db 61 IITAVSVVFFVGLVGNLSLVMFVIRYTKMKTATNIYIFNLALDALVTTMPFQSAVYL 120
QY 61 IITAVSVVFFVGLVGNLSLVMFVIRYTKMKTATNIYIFNLALDALVTTMPFQSAVYL 120
Db 121 mmswpgdvclckivlsidyymfcsifltmmsvdyriavchpkaIdfrtPlkakini 180
QY 121 MNSWPFQGVLCIKIVISIDYNNFTSIFTLTMSVDRYIAVCHPKAIdFRTPPLAKIINI 180
Db 181 ciwllssvgsaisaivlggtkrvedvylecslgfppddesvwdlfmkicvfiifaivpvl 240
QY 181 CIWLLASSVGSISAIVLGGTKRVEDVYLECSLGFPPDDEYSWMDLFMKICVFFAFVAPVYL 240
Db 241 IITVCYTLMLIRLKSVALLSGSRKEDNLRITKLVVAVAFITCWPPIHIFLIVBALG 300
QY 241 IITVCYTLMLIRLKSVALLSGSRKEDNLRITKLVVAVAFITCWPPIHIFLIVBALG 300
Db 301 stshstaalsyyfcialgytnsslnpvlvafidenfkrcfrdcfplkmmerqstsr 360
QY 301 STSHSTAALSSYYFCIALGYTNSLNPLVYAFIDENFKRCFRDCEFPKMKMERQSTNRV 360
Db 361 rntvqdpasmrdivgmnkpv 380
QY 361 RNTVQDPASMRDIVGGMKNKPV 380

```

```

RESULT 4
ENTRY JC2338 #type complete
TITLE kappa opioid receptor - human
ORGANISM Homo sapiens #common_name man
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
05-Jan-1996

ACCESSIONS
REFERENCE JC2338; A55354
#authors Mansson, E.; Bare, L.; Yang, D.
#journal Biochem. Biophys. Res. Commun. (1994) 202:1431-1437
#title Isolation of a human kappa opioid receptor cDNA from placenta.
#accession J02338
#molecule_type mRNA
#residues 1-380 #label MAN
#experimental_source placenta
REFERENCE A55354
#authors Wang, J.B.; Johnson, P.S.; Wu, J.M.; Wang, W.F.; Uhli, G.R.
#journal J. Biol. Chem. (1994) 269:25966-25969
#title Human kappa opiate receptor second extracellular loop elevates dynorphin's affinity for human mu/kappa chimeras.
#accession A55354
#status preliminary
#molecule_type mRNA
#residues 136-279 #label MAN
#cross-references GB:L36130
COMMENT This receptor preferentially binds to dynorphins.
KEYWORDS receptor; transmembrane protein
FEATURE
60-85 #domain transmembrane #status predicted #label TM1
95-114 #domain transmembrane #status predicted #label TM2
133-154 #domain transmembrane #status predicted #label TM3
177-199 #domain transmembrane #status predicted #label TM4
228-251 #domain transmembrane #status predicted #label TM5
275-296 #domain transmembrane #status predicted #label TM6
311-333 #domain transmembrane #status predicted #label TM7
SUMMARY #length 380 #molecular_weight 42659 #checksum 8304

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```

Query Match 96.8%; Score 2747; DB 13; Length 380;
Best Local Similarity 93.9%; Pred. No. 0.00e+00;
Matches 357; Conservative 17; Mismatches 6; Indels 0; Gaps 0;

```

```

Db 1 mmswpgdvclckivlsidyymfcsifltmmsvdyriavchpkaIdfrtPlkakini 60
QY 1 MESPLOIFRGDGPFCPSACILPNSSSWFPMAESDSNGSGSEDOQLESASHIPALPV 60

```

```

Db 61 IITAVSVVFFVGLVGNLSLVMFVIRYTKMKTATNIYIFNLALDALVTTMPFQSAVYL 120
QY 61 IITAVSVVFFVGLVGNLSLVMFVIRYTKMKTATNIYIFNLALDALVTTMPFQSAVYL 120
Db 121 mmswpgdvclckivlsidyymfcsifltmmsvdyriavchpkaIdfrtPlkakini 180
QY 121 MNSWPFQGVLCIKIVISIDYNNFTSIFTLTMSVDRYIAVCHPKAIdFRTPPLAKIINI 180
Db 181 ciwllssvgsaisaivlggtkrvedvylecslgfppddesvwdlfmkicvfiifaivpvl 240
QY 181 CIWLLASSVGSISAIVLGGTKRVEDVYLECSLGFPPDDEYSWMDLFMKICVFFAFVAPVYL 240
Db 241 IITVCYTLMLIRLKSVALLSGSRKEDNLRITKLVVAVAFITCWPPIHIFLIVBALG 300
QY 241 IITVCYTLMLIRLKSVALLSGSRKEDNLRITKLVVAVAFITCWPPIHIFLIVBALG 300
Db 301 stshstaalsyyfcialgytnsslnpvlvafidenfkrcfrdcfplkmmerqstsr 360
QY 301 STSHSTAALSSYYFCIALGYTNSLNPLVYAFIDENFKRCFRDCEFPKMKMERQSTNRV 360
Db 361 rntvqdpasmrdivgmnkpv 380
QY 361 RNTVQDPASMRDIVGGMKNKPV 380

```

```

RESULT 5
ENTRY I57005 #type complete
TITLE kappa opioid receptor - human
ORGANISM Homo sapiens #common_name man
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
02-Jul-1996

ACCESSIONS
REFERENCE I57005
#authors Zhu, J.; Chen, C.; Xue, J.
#journal Life Sci. (1995) 56:201-207
#title Cloning of a human kappa opioid receptor from the brain.
#accession I57005
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-380 #label RES
#cross-references GB:J37362; NID:g722617; CDS_PID:g722618
GENETICS
SUMMARY #length 380 #molecular_weight 42645 #checksum 8302

```

```

Query Match 96.7%; Score 2746; DB 13; Length 380;
Best Local Similarity 93.7%; Pred. No. 0.00e+00;
Matches 356; Conservative 18; Mismatches 6; Indels 0; Gaps 0;

```

```

Db 1 mmswpgdvclckivlsidyymfcsifltmmsvdyriavchpkaIdfrtPlkakini 60
QY 1 MESPLOIFRGDGPFCPSACILPNSSSWFPMAESDSNGSGSEDOQLESASHIPALPV 60
Db 61 IITAVSVVFFVGLVGNLSLVMFVIRYTKMKTATNIYIFNLALDALVTTMPFQSAVYL 120
QY 61 IITAVSVVFFVGLVGNLSLVMFVIRYTKMKTATNIYIFNLALDALVTTMPFQSAVYL 120
Db 121 mmswpgdvclckivlsidyymfcsifltmmsvdyriavchpkaIdfrtPlkakini 180
QY 121 MNSWPFQGVLCIKIVISIDYNNFTSIFTLTMSVDRYIAVCHPKAIdFRTPPLAKIINI 180
Db 181 ciwllssvgsaisaivlggtkrvedvylecslgfppddesvwdlfmkicvfiifaivpvl 240
QY 181 CIWLLASSVGSISAIVLGGTKRVEDVYLECSLGFPPDDEYSWMDLFMKICVFFAFVAPVYL 240
Db 241 IITVCYTLMLIRLKSVALLSGSRKEDNLRITKLVVAVAFITCWPPIHIFLIVBALG 300
QY 241 IITVCYTLMLIRLKSVALLSGSRKEDNLRITKLVVAVAFITCWPPIHIFLIVBALG 300
Db 301 stshstaalsyyfcialgytnsslnpvlvafidenfkrcfrdcfplkmmerqstsr 360
QY 301 STSHSTAALSSYYFCIALGYTNSLNPLVYAFIDENFKRCFRDCEFPKMKMERQSTNRV 360

```

Db	361	Envgdbp1rldidgmkpv	380
QY	361	ENVDPPASMRDVGGMKPV	380
RESULT	5		
ENTRY	A55259	#type complete	
TITLE	kappa opioid receptor - guinea pig		
ALTERNATE_NAMES	dynorphin receptor		
ORGANISM	#formal_name <i>Canis porcellus</i> #common_name guinea pig		
DATE	06-Feb-1995	#sequence_revision 06-Feb-1995	#text_change
ACCESSIONS	A55259		
REFERENCE	A55259		
#authors	Xie, G.; Meng, F.; Watson, A.; Thompson, R.C.; Hoversten, M.T.; Goldstein, A.; Watson, S.J.; Kiki, H.		
#journal	Proc. Natl. Acad. Sci. U.S.A. (1994) 91:3779-3783		
#title	Primary structure and functional expression of a guinea pig kappa opioid (dynorphin) receptor.		
#accession	A55259		
##status	preliminary		
##molecule_type	mRNA		
##residues	1-380	#label X1E	
##cross-references	GB:004092		
KEYWORDS	transmembrane protein		
SUMMARY	#length 380 #molecular-weight 42736 #checksum 7081		
Query Match	91.9%;	Score 2610;	DB 14; Length 380;
Best Local Similarity	92.9%;	Pred. No. 0.00e+00;	
Matches 338;	Conservative 21;	Mismatches 5;	Indels 0; Gaps 0
Db	17	arnacilpnsgsawljpwaeedngsqapqdeglepahispaipviltaysvvfvvglyg	76
QY	17	SSACILPSSSWFPMWASDSGVSQESHSISALPVILTAYSVVFEVGLVG	76
Db	77	nsllwfvilrrytkmkaatniyifnlaladalavtttmfpgsvylymswfpfdvklktivs	136
QY	77	NSLWVFIIRTKMTATNIYIFNLALDALVTTMFPQSAVLYMSWFPDVLCKIVIS	136
Db	137	ldgymmfteifcltumsvdylaavchpvaldrtfclakhlidclwlssvysaeail	196
QY	137	LDYNNFTSIFLITLMSVRYLAVCHPVALDRTPKAKIINICLWLLSSVGSISALVL	196
Db	197	ggtkyrvetdiiecsyqfdddysswdlfnklcvfyafayipvllilvocytlmlrlksv	256
QY	197	GGTKRVEDYIECSYQFPDDDESWMDLKKLCVFPAYFPIVLLIIVCYTLMILRLKSV	256
Db	257	rlsgrsekdrnlrlrlrlvllvvavflilwcpbhlfilvealgssthsaaalsyyfcl	316
QY	257	RLSGREKDRNLRRLRIKVLVAVVAFIILWPIHIFILVEAAGSTHSAAALSYYFCL	316
Db	317	algytusslnpilyaflidenfkccfdcfpikmergstsrvrtvgpaymrvndv	376
QY	317	ALGYTSSLNPPVLYAFIDENFKCFDFCEFPKIKRMKRGOSTNRYRNTVQDPASRDVGGM	376
Db	377	nkpy 380	
QY	377	NKPY 380	
RESULT	7		
ENTRY	S65693	#type complete	
TITLE	opioid receptor mu variant MORLA - human		
ORGANISM	#formal_name <i>Homo sapiens</i> #common_name man		
DATE	12-Jul-1996	#sequence_revision 26-Jul-1996	#text_change
ACCESSIONS	S65693; S51216		
REFERENCE	S65693		
#authors	Bare, L.A.; Mansson, E.; Yang, D.		
#submission	submitted to the EMBL Data Library, July 1994		
#description	Expression of two variants of the human mu opioid receptor mRNA in SK-N-SH cells and human brain.		

```

#accession S65693
##molecule_type mRNA
##residues 1-392 ##label BAR
##cross-references EMBL:U12569
REFERENCE
#authors Bare, L.A.; Mansson, E.; Yang, D.
#journal FEBS Lett. (1994) 354:213-216
#title Expression of two variants of the human mu opioid receptor
#mRNA in SK-N-SH cells and human brain.
#accession S51216
##molecule_type mRNA
##residues 387-392
SUMMARY
#length 392 #molecular_weight 43939 #checksum 6977

Query Match 59.2%; Score 1680; DB 13; Length 392;
Best Local Similarity 65.0%; Pred. No. 1,566-244;
Matches 210; Conservative 53; Mismatches 56; Indels 4; Gaps 4;

Db 70 attmalysicvaylfnflmyayivrvtkmktatniylfnaladalatslbfqsvn 129
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 59 PYIIIAVSVFVVGVLGNSLVMFIIIRTKMKATFNITIFMLADALVETTFEFGSAV 118
130 ylmgtwpgflllcklvisldyymfslsftlctmsvdyriavchpykaldftpnak:i 189
119 YLMNSMPGADVCKIKVISIDYNNMFTSFTLLTMSVDRIAVCHPKALDEFRLPKAKIT 178
Db 150 nvcnmlslssagldpwmfiatcktygg-s-ldctltfshptw-ywenllkicvfi:afmp 246
179 NCIICMLSSVVISKSLVAGIKVREVDVIESCLQPFDDFEYSWMDLFMKICVFVFEVLP 238
QY 247 VLIITCVGJMLIRLKSVMILSGSKednrlrrltmvlvrvavfvcwcpbhiylvlika 306
239 VLIITCVTLMILRLKSVMLSSGRKDNLRITKTLVYVAVFLICWPIHIFILVBA 298
Db 307 lvtlpettfgvswfhcialsytnscldpvlvafidntkrcfrefcslptssn:iequnt 366
QY 299 LGSTSHRALSSYFICALGYTNSSLNPNVLAFLDENFRKCRDPCFP:TKMKRQOSTN 358
Db 367 rlrqtrtdhrpstantcydrtnhq 389
QY 359 RVRNTVQD-PASMRDVGGMKKFP 380

RESULT 8
ENTRY A57510 #type complete
TITLE mu opioid receptor - mouse
ORGANISM Mus musculus #common_name house mouse
DATE 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 15-Oct-1996
ACCESSIONS A57510; I48665; I49300
REFERENCE A57510
#authors Kaufman, D.L.; Keith Jr., D.E.; Anton, B.; Tian, J.;
Maguendo, K.; Newman, D.; Tran, T.H.; Lee, D.S.; Wen, C.;
Xia, Y.R.; Lunsis, A.J.; Evans, C.J.
#journal J. Biol. Chem. (1995) 270:15877-15883
#title Characterization of the murine mu opioid receptor gene.
#accession A57510
#status nucleic acid sequence not shown
##molecule_type mRNA
##residues 1-398 ##label KAU
##cross-references GB:U19380
REFERENCE I48665
#authors Min, B.H.; Augustin, L.B.; Felsheim, R.F.; Fuchs, J.A.; Loh,
H.H.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:9081-9085
#title Genomic structure analysis of promoter sequence of a mouse mu
opioid receptor gene.
#accession I48665
#status translated from GB/EMBL/DBJ
##molecule_type DNA
##residues 1-398 ##label RES
##cross-references EMBL:U10561; NID:g555696; CDS_PID:g565069

```

REFERENCE I49300
#authors Rossi, G.C.; Pan, Y.X.; Brown, G.P.; Pasternak, G.W.
#journal FEBS Lett. (1995) 369:192-196
#title Antisense mapping the MOR-1 opioid receptor: evidence for alternative splicing and a novel morphine-6 beta-glucuronide receptor.
#cross-references M01D:95377399
#accession I49300
#status
#molecule-type mRNA translated from GB/EMBL/DBJ
#residues 1-398 ##label RE2
#cross-references EMBL:U26915; NID:g1055230; CDS_PID:g1055231
GENETICS
#introns 95/2: 213/1: 386/3
#note gene name MOR
KEYWORDS alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein
SUMMARY #length 398 #molecular-weight 44421 #checksum 8164
Query Match 59.1%; Score 1678; DB 14; Length 398;
Best Local Similarity 65.8%; Pred. No. 3.32e-244;
Matches 208; Conservative 55; Mismatches 49; Indels 4; Gaps 4;
Db 68 altimalysivcvglfqnfivmyvlyrvytkmktatnlyifnlaladalastlpfgsyn 127
QY 59 PVLITAVSVVGVGVGIVGNSLVMVIRITKMKATNTIIFNLADLVTTMPFOSAV 118
Db 128 ylmgtwpgfllckivlsidynmfstifcltmsvdrylavchpvaldftrpnaki 187
QY 119 YLMSWPGDYLCKIVISIDYNNFTSIFLLTMSVDRYLAVCHVYKALDFTRPNAKKI 178
Db 188 nycnwllssalgplpymfmatckyrqg-s-ldccltfshptw-ywenllkicvffafimp 244
QY 179 NICTMLASSVGSIAIVLGKIVKREDVDVIECSIQPFDEYSWMDLFCVFAFAVIP 238
Db 245 vllitvcygmllrlksvmlsgskednrlrrltlmvlyvavaficwtpihlyvika 304
QY 239 VLIITVCYTMILRLKSVRLSGSKEDRNLRLTKLVVAVAFICWTPIHFIIVEA 298
Db 305 lvtlptctftvshfclalgytncslpnylafldenfkrcfrcfclptsleqnsa 364
QY 299 LGSHTSHALSSYFICIALGYTNSLNPVLYAFLDENFKRCRDFCPDKMREROSTN 358
Db 365 rlrqnrtrhpsstanty 380
QY 359 RVR-NTVODPASMEDV 373
RESULT 9
ENTRY I56553 #type complete
TITLE opiate receptor mu - human
ALTERNATE_NAMES MOR1 protein; opioid receptor mu
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 06-Sep-1996
ACCESSIONS I56553; A38991; S41075; S51215
REFERENCE I56553
#authors Meszler, A.; Hurley, J.H.; Bye, L.S.; Campbell, A.D.; Chen, Y.; Tian, M.; Liu, J.; Schulman, H.; Yu, L.
#journal J. Neurosci. (1995) 15:2396-2406
#title The human mu opioid receptor: modulation of functional desensitization by calcium/calmodulin-dependent protein kinase and protein kinase C.
#cross-references M01D:95198115
#accession I56553
#status
#molecule-type mRNA translated from GB/EMBL/DBJ
#residues 1-400 ##label RES
#cross-references GB:I29301; NID:g459831; CDS_PID:g459832
REFERENCE A38991
#authors Wang, J.B.; Johnson, P.S.; Persico, A.M.; Hawkins, A.L.;

#submission Griffith, C.A.; Uhl, G.R.
#accession submitted to GenBank, August 1994
#status A38991
#molecule-type mRNA translated from GB/EMBL/DBJ
#residues 1-50, 'N', 52-233, 'V', 235-400 ##label WAN
#cross-references GB:I25119; CDS_PID:g452073
S41075
#authors Wang, J.B.; Johnson, P.S.; Persico, A.M.; Hawkins, A.L.; Griffith, C.A.; Uhl, G.R.
#journal FEBS Lett. (1994) 338:217-222
#title Human mu opiate receptor. cDNA and genomic clones, pharmacologic characterization and chromosomal assignment.
#accession S41075
#status
#molecule-type mRNA translated from GB/EMBL/DBJ
#residues 1-50, 'N', 52-400 ##label WA2
REFERENCE S51215
#authors Bare, L.A.; Mansson, E.; Yang, D.
#journal FEBS Lett. (1994) 354:213-216
#title Expression of two variants of the human mu opioid receptor mRNA in SK-N-SH cells and human brain.
#accession S51215
#status preliminary
#molecule-type mRNA
#residues 387-400 ##label BAR
GENETICS
#gene GDB:OPRMI
#cross-references GDB:137216
#map_position 6q24-6q25
KEYWORDS G protein-coupled receptor; glycoprotein; transmembrane protein
FEATURE
73-96 #domain transmembrane #label TM1\
107-132 #domain transmembrane #label TM2\
144-165 #domain transmembrane #label TM3\
188-208 #domain transmembrane #label TM4\
236-257 #domain transmembrane #label TM5\
283-304 #domain transmembrane #label TM6\
323-342 #domain transmembrane #label TM7\
9,12,33,40,48 #binding_site carbohydrate (Asn) (covalent) #status predicted
SUMMARY #length 400 #molecular-weight 44779 #checksum 3741
Query Match 59.1%; Score 1677; DB 13; Length 400;
Best Local Similarity 66.6%; Pred. No. 4.84e-244;
Matches 207; Conservative 52; Mismatches 49; Indels 3; Gaps 3;
Db 70 altimalysivcvglfqnfivmyvlyrvytkmktatnlyifnlaladalastlpfgsyn 129
QY 59 PVLITAVSVVGVGVGIVGNSLVMVIRITKMKATNTIIFNLADLVTTMPFOSAV 118
Db 130 ylmgtwpgfllckivlsidynmfstifcltmsvdrylavchpvaldftrpnaki 189
QY 119 YLMSWPGDYLCKIVISIDYNNFTSIFLLTMSVDRYLAVCHVYKALDFTRPNAKKI 178
Db 190 nycnwllssalgplpymfmatckyrqg-s-ldccltfshptw-ywenllkicvffafimp 245
QY 179 NICTMLASSVGSIAIVLGKIVKREDVDVIECSIQPFDEYSWMDLFCVFAFAVIP 238
Db 247 vllitvcygmllrlksvmlsgskednrlrrltlmvlyvavaficwtpihlyvika 306
QY 239 VLIITVCYTMILRLKSVRLSGSKEDRNLRLTKLVVAVAFICWTPIHFIIVEA 298
Db 307 lvtlptctftvshfclalgytncslpnylafldenfkrcfrcfclptsleqnsa 365
QY 299 LGSHTSHALSSYFICIALGYTNSLNPVLYAFLDENFKRCRDFCPDKMREROSTN 358
Db 367 rlrqnrtrhps 377
QY 359 RVR-NTVODPASMEDV 369

[illegible]

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DATE                26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
ACCESSIONS         06-Sep-1996
REFERENCE          156517; 157951
#authors           Bunzow, J.R.; Zhang, G.; Bouvier, C.; Saez, C.; Ronneklev, O.K.; Kelly, M.J.; Grandy, D.K.
#journal            J. Neurochem. (1995) 64:14-24
#title              Characterization and distribution of a cloned rat mu-opioid receptor
#cross-references   MUID:95096825
#accession          156517
#status             preliminary; translated from GB/EMBL/DDBJ
#molecule_type     mRNA
#residues            1-398 #label RNS
#cross-references   EMBL:U02083; NID:g403573; CDS_PID:g403574
REFERENCE           157951
#authors            Chen, Y.; Westek, A.; Liu, J.; Hurley, J.A.; Yu, L.
#journal            Mol. Pharmacol. (1993) 44:8-12
#title              Molecular cloning and functional expression of a mu-opioid receptor from rat brain.
#cross-references   MUID:93341493
#accession          157951
#status             preliminary; translated from GB/EMBL/DDBJ
#molecule_type     mRNA
#residues            1-398 #label RE2
#cross-references   GB:L13069; NID:g348250; CDS_PID:g348251
SUMMARY             #length 398 #molecular_weight 44508 #checksum 8374

Query Match        59.0%; Score 1674; DB 14; Length 398;
Best Local Similarity 65.8%; Pred. No. 1.50e-243;
Matches 208; Conservative 54; Mismatches 50; Indels 4; Gaps 4;

Db      68 attlnalsivcvglfgnflvmylvirytkmktamlyifnlaladaatsrlpgsqvn 127
       ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      59 pvlitavysvvvgvghvgnslvmfviirkmtkntaniiftnlaladavlttmpposav 118
       ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Db      128 ymgwpfpftllckivlsidyymftsiftlcumsdyriavchpykaldfrrpnakiv 187
       |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      119 ylmnswpfedvlocklvisldiyimfssittltmmsadvriaichpkaldfrplakrit 178
       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Db      188 nvcwnwlssaqlgipwfmattkyrg-s-idcltfsptw-ywenllkicvfifaimp 244
       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      179 nictmwllasvgsaivlogtkrvdevdiessloqppdpeyswmwdlfmkicvvefavip 238
       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Db      245 lllltwcylmlilksvzmjlsgskcdnrlritcmwlvvaavfiocwtphihylila 304
       :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      239 viilitcytlmlrlksvyrllsgsrkdnmrlarkitklavlvaavfiicwtpihffileea 298
       :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Db      305 lltipettfgtwshciaigyfnscnplylaflenfkrcrfecioesltseqtgnst 364
       :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      299 tgstshstalssryfcialgytnsslmpvlpfldenkrccrdpcfpikmrkerostin 358
       :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Db      365 ryvrqnrehpstanty 380
       |||||::|::|::|
QY      359 rvr-nivqpdsrmdy 373
       |||||::|::|::|

RESULT            12
ENTRY             156504 #type complete
TITLE             mu opioid receptor - rat
ORANISM            #forml_name Rattus norvegicus #common_name Norway rat
DATE              26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
ACCESSIONS        156504
REFERENCE          156504
#authors           Zastany, R.L.; George, S.R.; Nguyen, T.; Cheng, R.; Tsatsos, J.; Briones-Urbina, R.; O'Dowd, B.E.
#journal            J. Neurochem. (1994) 62:2099-2105
#title              Cloning, characterization, and distribution of a mu-opioid receptor in rat brain.
#cross-references   MUID:94246380
#accession          156504
#status            preliminary; translated from GB/EMBL/DDBJ

```

```

##molecule_type mRNA
##residues 1-398 ##label RES
##cross-references EMBL:U35424; NID:g40107731; CDS_PID:g40107732
SUMMARY #length 398 #molecular_weight 44403 #checksum 8604

Query Match
Best Local Similarity 58.4%; Score 1659; DB 14; Length 398;
Matches 208; Conservative 53; Mismatches 51; Indels 4; Gaps 4;

Db 68 altmalysvcvvglgfngflmvyivryckmkatnlyfnaladalatslpfgsvn 127
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 59 pvtitavysvfvvgvlgvnsllmfvilrktmkatnlyfnaladalatslpfgsav 118
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 128 ylmgtwpgfctllckivysidymnfstfictmsvgrylavchpvykaldftrpnakiv 187
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 119 ylmmswefgvlckivysidymnfstfictmsvgrylavchpvykaldftrpnakii 178
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 188 nvcnwllssaisglpvmfmattkyrg-s-ldcttlfshpew-ywenllkiovgfatimp 244
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 179 nciwllassvgisatylggtkvrddvylecslqfpdderxswmdlpmkicvfevavip 238
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 245 vllitvcygmllrlfksvymllsgskednrlrrlttmvlyvavfivcwprhlyvlla 304
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 239 vllitvcygmllrlfksvymllsgskednrlrrlttmvlyvavfivcwprhlyvlla 298
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 305 lltipettfgtswhefcialgyfnsclnplylaflgenfkrctrefcipsstlegust 364
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 299 lgstststalsstfycialgynsslnpvlafldbnrfcrdpcfpikmmerostn 358
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 365 ryrqntrephstanty 380
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 359 rvr-ntvdpasmdv 373
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
ENTRY 138657 #type complete
TITLE delta opiate receptor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
ACCESSIONS 138657
REFERENCE 138657
#authors Simonin, F.; Befort, K.; Gaveriaux-Ruff, C.; Matthes, H.;
#journal Napprey, V.; Janes, B.; Michelletti, G.; Kieffer, B.
#title Mol. Pharmacol. (1994) 46:1015-1021
#molecule_type mRNA
#cross-references EMBL:U35424; NID:g40107731; CDS_PID:g40107732
#accession 138657
#status preliminary; translated from GB/EMBL/DBJ
#residues 1-372 ##label RES
#cross-references EMBL:U35424; NID:g40107731; CDS_PID:g40107732
SUMMARY #length 372 #molecular_weight 40368 #checksum 1668

Query Match
Best Local Similarity 56.8%; Score 1612; DB 13; Length 372;
Matches 217; Conservative 60; Mismatches 58; Indels 9; Gaps 8;

Db 15 lfnasdayps-a-cpsaganaagppgarsas-sialaialatalsavcayglignvlym 71
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 22 lfnssswfepnwmaesdsngsvsedqolesahispaipvitiavysvfvvgvlgvnsllm 81
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 72 fgivryckmkatnlyfnaladalatslpfgsakylmetwpgelickavsisdyyn 131
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 82 fvliirytmkatnlyfnaladalatslpfgsakylmetwpgelickavsisdyyn 141
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 132 mftisflltmmsvdyrlavchpvykaldftrpnakllnicicwlasgyvdimwavntrp 191
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 142 mftisflltmmsvdyrlavchpvykaldftrpnakllnicicwlasgyvdimwavntrp 191
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 192 rdga-vv-cltqfbsp--swydwctvkicovflfaivpdliltvcygmllrlfksvlls 247
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 202 REDVDVLECSHQFPDDEYSW-WDLFMKICVFEVFAVPIVITLITCYTLMIRLSVLLS 260
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 248 gskednrlrrlttmvlyvavfivcwprhlyvllaflgenfkrctrefcipsstlegust 307
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 261 gskednrlrrlttmvlyvavfivcwprhlyvllaflgenfkrctrefcipsstlegust 319
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 308 yansslapvlyafldenfkrcfrglc-kpogrpssfstarea 351
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 320 ytnsslnpvlafldbnrfcrdpcfpikmmerostnrvnt 363
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14
ENTRY 334592 #type complete
TITLE delta opiod receptor - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change
ACCESSIONS 334592
REFERENCE 334592
#authors Fukuda, K.; Kato, S.; Mori, K.; Nishi, M.; Takeshima, H.
#journal FEBS Lett. (1993) 327:311-314
#title Primary structures and expression from cDNAs of rat opiod
#accession 334592
#molecule_type mRNA
#residues 1-372 ##label FUK
REFERENCE 156571
#authors Aboud, M.E.
#journal J. Neurosci. Res. (1994) 27:714-719
#title Molecular cloning and expression of a rat delta opiod
#molecule_type mRNA
#accession 156571
#status preliminary; translated from GB/EMBL/DBJ
#residues 1-372 ##label RES
#cross-references EMBL:U00475; NID:g403488; CDS_PID:g514211
GENECS 156571
SUMMARY #length 372 #molecular_weight 40449 #checksum 2221

Query Match
Best Local Similarity 56.7%; Score 1610; DB 14; Length 372;
Matches 214; Conservative 55; Mismatches 48; Indels 9; Gaps 7;

Db 15 lfnasdayps-a-cpsaganaagppgarsas-sialaialatalsavcayglignvlym 71
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 22 lfnssswfepnwmaesdsngsvsedqolesahispaipvitiavysvfvvgvlgvnsllm 81
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 72 fgivryckmkatnlyfnaladalatslpfgsakylmetwpgelickavsisdyyn 131
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 82 fvliirytmkatnlyfnaladalatslpfgsakylmetwpgelickavsisdyyn 141
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 132 mftisflltmmsvdyrlavchpvykaldftrpnakllnicicwlasgyvdimwavntrp 191
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 142 mftisflltmmsvdyrlavchpvykaldftrpnakllnicicwlasgyvdimwavntrp 191
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 192 rdga-vv-cltqfbsp--swydwctvkicovflfaivpdliltvcygmllrlfksvlls 247
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 202 REDVDVLECSHQFPDDEYSW-WDLFMKICVFEVFAVPIVITLITCYTLMIRLSVLLS 260
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 248 gskednrlrrlttmvlyvavfivcwprhlyvllaflgenfkrctrefcipsstlegust 307
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 261 gskednrlrrlttmvlyvavfivcwprhlyvllaflgenfkrctrefcipsstlegust 319
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 308 yansslapvlyafldenfkrcfrglc-kpogrpssfstarea 351
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 320 ytnsslnpvlafldbnrfcrdpcfpikmmerostnrvnt 363
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 15
ENTRY B48227 #type complete
TITLE delta opiod receptor 1 - mouse

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ORGANISM      #formal_name Mus musculus #common_name house mouse
DATE          26-May-1994 #sequence_revision 26-May-1994 #text_change
              01-Dec-1995
ACCESSIONS    B48227; S37807; A48685
REFERENCE     A48227
#authors      Yasuda, K.; Raynor, K.; Kong, H.; Breder, C.D.; Takeeda, J.;
#journal      Reisine, T.; Bell, G.I.
#title        Proc. Natl. Acad. Sci. U.S.A. (1993) 90:6736-6740
              Cloning and functional comparison of kappa and delta opioid
              receptors from mouse brain.
#accession    B48227
#status       preliminary
#molecule_type mRNA
#residues     1-372 #label YAS
#cross-references GB:LI1064

REFERENCE     S37807
#authors      Kieffer, B.L.; Befort, K.; Gaveriaux-Ruff, C.; Hirth, C.G.
#submission   submitted to the EMBL data library, February 1993
#accession    S37807
#status       preliminary
#molecule_type mRNA
#residues     1-372 #label KIE
#cross-references EMBL:L06322

REFERENCE     A48685
#authors      Bzdega, T.; Chin, H.; Kim, H.; Jung, H.H.; Kozak, C.A.; Klee,
              W.A.
#journal      Proc. Natl. Acad. Sci. U.S.A. (1993) 90:9305-9309
#title        Regional expression and chromosomal localization of the delta
              opiate receptor gene.
#cross-references MJD:9402364
#accession    A48685
#status       preliminary
#molecule_type mRNA
#residues     8-372 #label BZD
#cross-references NCBI:138618; NCBI:138619
#experimental_source NG108-15 hybrid cells
#note         sequence extracted from NCBI backbone
              brain; G protein-coupled receptor; glycoprotein;
              phosphoprotein; transmembrane protein
KEYWORDS      #length 372 #molecular-weight 40561 #checksum 3372

SUMMARY
Query Match      56.3%; Score 1597; DB 14; Length 372;
Best Local Similarity 66.7%; Pred. No. 6,11e-231;
Matches 206; Conservative 51; Mismatches 46; Indels 6; Gaps 5;

Db 47 alaataalsavcavglgnvltmfgivrytktkatniyifnlaladalatslfpqs 106
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 57 alpvtltavsvfvvlgvngslvmevltitrtkmtatnltitfnlaladalvttmfpqs 116
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 107 akylmetwfpfgellckavlsldymnftslftlmsvdrtyiavchpvakaldftrpakak 166
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 117 avylmmswpgdvckvlsidyytmetsifltlmsvdrtyiavchpvakaldftrpakak 176
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 167 lndiclwlasvgvvpimwmatvqprda-vv-cmlqfbsp--swywdvtvklcovflfaf 222
   :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 177 iiniciwllassvgisaiyvggkvredvdvicslqfpdexsw-wdlfmklcovevfaaf 235
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 223 vvpdlititvcygmllrlrsrllsgskedrsllrtitrmvlvvvgaftvccwapihlfvi 282
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 236 vipvlititvcytmllrlksvrlslsgsrekdrnrlrttkllyvvavfllcwpdihffil 295
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 283 vwtlvdnrrdpiwvaalhhcjalgyansslmpvlyafidenfkrctqqlortpcgrqep 342
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 296 vnalgstshsta-alsstycialgytnsslnpvlvafldnenfkrctqqlortpcgrqep 354
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 343 gslrrprqa 351
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 355 qstnrvrnt 363
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

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Search completed: Tue Aug 26 14:52:07 1997
 Job time : 104 secs.


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QY 170 AGCTGACGCGTCACCAATGAGTCCGCCATTCAGATCTCCGAGAGATCCAGCCCTAC 229
Db 155 CTGTGCTCCAGTGTCTCTACCTCCGCAAGAGCGCTGTGTTCCCAACTGGCGCA 214
QY 230 CTGCTCTCCAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 289
Db 215 ATCGGACGAAGTGGCAAGTGGGCTCGAGAGATGAGAGTGGAGTGGAGTGGAGTGG 274
QY 290 ATCGGACGAAGTGGCAAGTGGGCTCGAGAGATGAGAGTGGAGTGGAGTGGAGTGG 349
Db 275 TCCGAGCATCCCTGTATATACATCCGCGCTGTCTCTCTCTCTCTCTCTCTCTCTCT 334
QY 350 TCCGAGCATCCCTGTATATACATCCGCGCTGTCTCTCTCTCTCTCTCTCTCTCTCT 409
Db 335 GGGCAATCCCTGTATATACATCCGCGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 394
QY 410 GGGCAATCCCTGTATATACATCCGCGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 469
Db 395 CATACATATTAACCTGGCTTGGAGATGCTTGTCTCTCTCTCTCTCTCTCTCTCTCT 454
QY 470 CATACATATTAACCTGGCTTGGAGATGCTTGTCTCTCTCTCTCTCTCTCTCTCTCT 529
Db 455 GAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 514
QY 530 GAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 589
Db 515 TTCCATTTGACTACTACACATGTTTACACATTTTCCATTTTCCATTTTCCATTTTCC 574
QY 590 TTCCATTTGACTACTACACATGTTTACACATTTTCCATTTTCCATTTTCCATTTTCC 649
Db 575 CCGCTACATGCTGTGTGGCACCCTGGAAGCTTTGGAGTTCGGAACCTTTGGAAGC 634
QY 650 CCGCTACATGCTGTGTGGCACCCTGGAAGCTTTGGAGTTCGGAACCTTTGGAAGC 709
Db 635 AAGATCAATCAATCTGTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 694
QY 710 AAGATCAATCAATCTGTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 769
Db 695 CCGTGAAGCAACCAAGTGAAGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 754
QY 770 CCGTGAAGCAACCAAGTGAAGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 829
Db 755 TATATGATGATATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 814
QY 830 TATATGATGATATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 889
Db 815 TATATGATGATATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 874
QY 890 TATATGATGATATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 949
Db 875 TATATGATGATATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 934
QY 950 TATATGATGATATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1009
Db 935 TATATGATGATATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 994
QY 1010 TATATGATGATATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1069
Db 995 TATATGATGATATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1054
QY 1070 TATATGATGATATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1129
Db 1055 TATATGATGATATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1114
QY 1130 TATATGATGATATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1189
Db 1115 TATATGATGATATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1174
QY 1190 TATATGATGATATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1249
Db 1175 TATATGATGATATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1234
QY 1250 TATATGATGATATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1309

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Db 1225 GATGATTAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1294
QY 1310 GATGATTAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1369
Db 1295 GATGATTAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1335
QY 1370 GATGATTAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1410

RESULT 3
ID T12550 standard; cDNA; 1142 BP.
AC T12550;
DT 03-SEP-1996 (first entry)
DE Human kappa opiod receptor cDNA.
KW Human; kappa opiod receptor; psychiatric disorder; cardiovascular;
OS neurology; diagnosis; ds.
FH Homo sapiens.
FT Key Location/Qualifiers
FT CDS 1..1142
FT /tag= a
FT /product= kappa-opioid_receptor
FT /note= "incomplete termination codon"
PN M09601898-A1.
PD 25-JAN-1996.
PE 07-JUL-1995; F00912.
PR 11-JUL-1994; FR-008531.
PA (USTR-) UNIV. PASTEUR STRASBOURG LOUIS.
PI Kieffer B, Simonin F;
DR WPI; 96-097628/10.
PI P-PSDB; R88722.
PT New nucleic acid encoding the human kappa opiod receptor - useful
PT in diagnosis and therapy, and for isolating receptor ligands and
PT modulators
PS Claim 3: Page 13-15; 30pp; French.
CC This sequence codes for the human kappa opiod receptor and was
CC obtained from two overlapping cDNA fragments isolated from a
CC human placental cDNA library. The fragments were amplified from
CC the library using PCR primers based on the sequence of human
CC genomic clones which hybridised with a murine delta receptor cDNA
CC probe. Nucleotide probes derived from the kappa opiod receptor
CC coding sequence are useful for diagnosis of neurological, cardio-
CC vascular and psychiatric disorders associated with opiod
CC receptors.
SQ Sequence 1142 BP; 236 A; 337 C; 283 G; 286 T;

Query Match 59.4%; Score 838; DB 20; Length 1142;
Best Local Similarity 86.7%; Pred. No. 0.00e+00;
Matches 990; Conservative 0; Mismatches 152; Indels 0; Gaps 0;

```

Db	361	atgaatctcgtgaccttltggggatgctgtgtaagaatgaatattccattgatttacc	420
QY	546	ATGAATCTCTGGCCCTTTGGAGATGTCATAGCAAGATTCTCATTTTCCATTGACTACTAC	605
Db	421	aacatgttcaacaacacattccacttaccatgatagacgttgagacgctacattgcctgt	480
QY	606	AACATGTTTACACACATATTCACCTTGACCATGATGATGTGAGACCGCTACATGTGCTGTG	665
Db	481	tgcacaccccgtagaagccttggagcttcgcacaccccttgaaaggaagatcatcaatc	540
QY	666	TGCACACCCCTGTGAAGAGCTTTGGACTTCCGAACACCTTTGAAGAAAGATCATCAATC	725
Db	541	tgcactgtgctgcgtgtgtcatctgtttggacatctctcgaatagctcttggagaccaaa	600
QY	726	TGCATTTGGCTGCTGGCATCTCTGTGTGTTATACACGGAATAGTCCTTGGAGGACCAAA	785
Db	601	gtcaggagaagacgtcgaatgcatgatagatgctccttgcgaattcccaatgagactacc	660
QY	786	GTCAGGGAAGATGTGGATGCTATTGAAGATGCTCTTGCAAGTTTCTGTGATGATATTC	845
Db	661	tggtggagacctcttcaatgaasatcttgcttctcatcttttggctctcgtatcccgctctc	720
QY	846	TGTTGGGATCTCTTCATGAAATCTGTCTTCTGCTTTGCTTTGTGATCCAGTCCTC	905
Db	721	atcatcatcgtctgtctacacccctgtatctctgtcgtctcaagacgtctcggctcttct	780
QY	906	ATCATCATTTGCTGTACACCTTANATNCTGGCGCCGGAAGATGCTCGGCTCTGTCT	965
Db	781	ggtctccgagagaagaatcgaacctcgttagatgataccagactgtctctgtgtgtgtg	840
QY	966	GGCTCCCGAGAAAGACCCGAATCTCCGCGGCATCACCAAGCTGGTCTGTAGTAGTT	1025
Db	841	gaagcttcctgtctgtctgagctcccaattcaatcatcctgtgtgagagctctgag	900
QY	1026	GGAGCTTCATCATCTGTTGGACCCCCCATACACATCTTATTCCTGGTGAAGCTGTGGA	1085
Db	901	agcacctcccaagacagacagctgtctctccagctatctaacttctgatcgtccttaggctat	960
QY	1086	AACACCTCCCAAGACAGACAGCTCCCTCTCCACATTTTCTTGTGATTCGCTTGGGTTAT	1145
Db	961	accacaagtagcctgaatcccatctctctagcgccttcttgatgtaaaacttcaagcgtgt	1020
QY	1146	ACCAACAGACGCTGATCTGATCTTCTCTGATGGCTTTTCGGATGAAGAACTCTCAAGCGGTGT	1205
Db	1021	tcccggaacttctgcttccactgtaagatgagagatcgagacgagacactagcagatc	1080
QY	1206	TTTATGGGACCTTGGCTTCCCTATTAAGATGCGATGGAAGCCGACGACCAATAGAGTT	1265
Db	1081	cgaatcacagttcaagatcctgtcttaccctcagagaggaatcgaatgagtgtaataaaccaatg	1140
QY	1266	AGAAACACAGTTGAGATCTCTGTTCCATGAGAGATGTGGAGGAGTGAATTAAGCCAGTA	1325
Db	1141	tgt 1142	
QY	1326	TG 1327	
RESULT 4			
ID	Q75931 standard; DNA; 1000 BP.		
AC	Q75931;		
DE	18-AUG-1995 (first entry)		
DT	Human kappa opiod receptor partial cDNA fragment.		
KW	Mouse; kappa; delta; mu; opiod receptor; brain; primer; PCR; amplify;		
KW	transmembrane domain; somatostatin; receptor; human; expression vector		
KW	truncate; chimeric; assay; probe; ss.		
OS	Homo sapiens.		
FN	Key		
FT	Location/Qualifiers		
FT	FT CDS 102..989		
FT	/tag= a		
FT	/product= partial human kappa opiod receptor		
PN	W09428132-A.		
PD	08-DEC-1994.		

DB	Query Match	Best Local Similarity	Matches	789; Conservative	0; Mismatches	109; Indels	3; Gaps	2
DB	100	gatacaaaaagtgaagacagacagacaacattatcataatttaacctggttcgacatg	159					
QY	442	GATACCGAGAGTGAAGACCGACACACATATACATATTTTAACTGGCTTGGAGATG	501					
DB	160	cttagtactacaaccatgccccttcacagtagcgttactgtgaattccgtgcctt	219					
QY	502	CTTTGGTTACTACCACTATGACCTTTTACAGAGTGCTGTCTACTTGTATGATTTCTTGCCCTT	561					
DB	220	ttagggatgtgctgtgacagatagtaatttcattgattactacaacatgttcaccagca	279					
QY	562	TTGGAGATGTGCATGTCACAGATTTGTTATTTCCATTGACTACACACATGTTTACACGCA	621					
DB	280	tcttcaccttcacatgacgagacgttgaaocgtacacatgctgtgcccaccocctggaag	339					
QY	622	TATTCACCTTGACACAGATGAGTGGTGAACCGCTACATTTGCTGTGTGCCACCCCTGTGAAG	681					
DB	340	ctttggaacttcgcacaccccttgaaagaaagatacatatctgcactcgtcgtctgt	399					
QY	682	CTTTGGACTTCCACACACCTTTTGAAGCAAGATGATCTACACATCTGCCATTTGGCTCTCG	741					
DB	400	cgtcatcgttgcacatctcgtcgaatagtccttgtagagcaacaaagtcagggaggtgac	459					
QY	742	CATCATCTGTGTGTAATACGCCATATGTCTTGGAGGCACACAAAGTCAGGGAAGATGTGG	801					
DB	460	atgtcattgagtgcgttggtcaagttcccaagatgacgactaactccgtgtggaccttca	519					
QY	802	ATGTCAATTGAATGCTCTCTTGCATTTCTCATATGATGAATATTTCTGGTGGATCTTTCA	861					
DB	520	tgaagatcgtcgtcttcatcttcttgcccttgtaacccctgcctccatcatcatatgctgtc	579					
QY	862	TGAAGATCTGTGTTCTGTGTTTGGCTTTGTGATCCCAAGTCCATCATCATATGTCTGCT	921					
DB	580	acaccctgacgacatcgtcgtctcaagaaatgcgcctcttcttggtctcccgagagaag	639					
QY	922	ACACCTCGATGATCTGCTGGCCTGAAGAGTTCGGGCTCTGCTGTGGGCTCCGAGAGAGG	981					
DB	640	atnnaaactgcgttaggataccaagactggtcctgtgtgtgtgtgtgtgtgtgtgtgtc	699					
QY	982	ACCGAAATCTGCCGCGATCACCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1041					
DB	700	gtctgactccatcatcaatatatctctgtgtgaggtcctctggaggaacctcccaagca	759					
QY	1042	GTGTGACCCCATTCACATCTTTTCTCTGTGTGAGGCTCTGTGGAGACACCTCCACACGCA	1101					

```

ID      RESULT      5
AC      Q79199; standard; cDNA; 2070 BP.
DE      19-APR-1995 (first entry)
DI      Rat mu-subtype opioid receptor cDNA.
DS      Mu-subtype opioid receptor; MSOR; drug addiction; ds.
KW      Rattus rattus.
FH      Key
FT      CDS      Location/Qualifiers
FT      /tag= a
FT      /product= Mu-subtype_opioid_receptor
PN      EP-612845-A.
PD      31-AUG-1994.
PF      09-FEB-1994; 101968.
PR      26-FEB-1993; US-026140.
PA      (AMCY ) AMERICAN CYANAMID CO.
PI      Corbett MJ, Eppler CM, Shieh H, Zysk JR;
DR      WPI: 94-265963/33.
DR      P-PSDB: R65188.
PT      Pure mu-type opioid receptor protein - and nucleic acid coding
PT      for it
PS      Claim 1; Fig 11; 39PD; English.
PS      R65188 is the rat mu-subtype opioid receptor protein purified
CC      from rat brain membranes, with Biotinyl-b-endorphin (R5666)
CC      as its ligand. It is encoded by the nucleotide sequence Q79199
CC      which was synthesised using Q71022 and Q71023 as PCR primers.
CC      R65188 is useful for identifying other receptor subtypes, for
CC      screening new opioid ligands, and for studying mechanisms of
CC      opioid action, e.g. drug addiction.
SQ      Sequence 2070 BP; 526 A; 564 C; 423 G; 557 T;

```

Db 1/1 ttacacatcaaggcccttactcatctgctcgtttaaggagccctcttoggaaattctctg 230
 QY 364 TATTCATCAACCGCTGTCCTACTCTGTGATTTGTTGGTGGCTTAGTGGCAATTCCTGG 423
 Db 231 tctatgatgtgattgttaagatacaccanaatgaagatgcacacaatctacatttca 290
 QY 424 TCATGTTTGTCATCAATCCGATACACGAATGAAGACCGCAACATCTACATATTTA 483
 Db 291 acctgtctctggagaagcgttttaggaaccgttcaactgcctcttcagaagtgtcaactac 350
 QY 484 ACCTGCTTTGGCAGATGCTTTGGTTACTAACCACTATGCCCTTTAGAGAGCTGTCTACT 543
 Db 351 tgatggaaacatgagcccttcggagaccatccctcggagaatcgtgactcaataatgattact 410
 QY 544 TGTATGATCTTGGCTTTTGGAGATGCTCTAAGCAAGATGTCATTTCCATTGGAATTA 603

Db	411	aaacaatfttaccacgcgcatattaccacccctctacacagagcgtgtgagccgttaactgtc	470
QY	604	ACACATGTTTACCGACGACATTTACCTTGACCAAGATGAGTGGACCGCTACATTCTG	663
Db	471	tctgcaccacgaatcaagacccttgatttcgcgttacccccgaatgccaatatgtcaag	530
QY	664	TGCGCACCCCTGAAAGCTTTGAGCTTCCGAAACACCTTTGAAGCAAAATATATACAA	723
Db	531	tctgcacatgtatctctctctctctctctctgcacatcggctcgtccctgttaattgtcaatgcaaccaa	590
QY	724	TCGTGATTGGCTCCTCGGCATCATCTGTTGGTATATACGAGGATAGTCTTGAGGGACCA	783
Db	591	aataagagca-g-g-gg-tc-cataagtttgacccctcaagttctccaccacaacctggt	644
QY	784	AGTCACGGAGAGATGTGATGTCAATGTGATAGTCTCTCGAGTTTCCGTGATGATGAATAT	843
Db	645	actgg-gagaa-cctgc-tcaaaactggtccttatcttcgcttcatcgttcataatgcagctc	701
QY	844	CTGTGTGGATCTCTTCAAGAAATCTGTCTGCTTCTGCTTGTGCTTTGCTTTGATCCAGTCC	903
Db	702	tcatatcacgtgtgttaagcgtctgatgatcttaagaactcaagagcgttcagatgcat	761
QY	904	TGATCATATTTGTCTGTACACCTGTATGATCCGTGCGCCTGAAGAGATGTGCGGCTCTGT	963
Db	762	cgggctccaagaagaagacagagatcttgacagagatccacccagatggtgtgtgtgtg	821
QY	964	CTGGCTCCCGAAGAGAGCCGAAATCTCCGCGCATACCAAGAGTGCTGTGTGATG	1022
Db	822	tggcgtattatctgtctgtgtgaaccacaatcacatctaacgtcatcatcaaaagcgtga	881
QY	1024	TTGCGTCTTATATATCTGTTGGACCCCAATTCACATCTTATTCGTGAGGCGTCTGG	1083
Db	882	tcaagattccagaacacacattcaagcsgttctccgtgcaactctgcattgtcttgggt	941
QY	1084	GAGGACCTCCCAAGACACAGCACTGCTCTCCACGCTATTTCTGTATTTGGCTTGGGT	1143
Db	942	acaagaaagctgcctgaataacagttcttaagcctcttccttgatgtgaanaactcaagcgt	1001
QY	1144	ATACCAACAGAGCGCTGAATCCTGTCTGTATGCCCTTTTGATGAAATCTCAAGCGGT	1201
Db	1002	gcttcagagagttgatctccc	1023
QY	1204	GTTTtaaggacttctgttccc	1225

```

RESULT      6
ID          Q089222 standard; cDNA; 1618 BP.
AC          Q089222;
DT          20-OCT-1995 (first entry)
DE          Rat mu opioid receptor cDNA.
KW          Mu opioid receptor; MOR-1; gene therapy; diagnostic; ss.
OS          Rattus sp.
FH          Key
FT          Location/Qualifiers
FT          CDS
FT          /*tag= a
PN          WO9507983-A.
PD          23-MAR-1995.
PF          13-SEP-1994; U10358.
PR          13-SEP-1993; US-120601.
PA          (INDV ) UNITY INDIANA FOUND.
PI          Yu L;
DR          WPI; 95-131351/17.
DR          P-PDB; R71964.
PI          New nucleic acid encoding new human mu opioid receptor - and
PI          related vectors, transformed cells, antibodies etc., useful in
PI          diagnosis, treatment and drug screening.
PI          disclose; Page 190-194; 266pp; English.
CC          A 365 bp fragment of the mouse delta opioid receptor was used to
CC          screen a rat brain cDNA library under low stringency conditions.
CC          One positive clone included the sequence given in Q089222, encoding a
CC          mu opioid receptor, MOR-1 (R71964). MOR-1 was stably expressed in
CC          transfected CHO cells.
CC          Sequence 1618 BP; 390 A; 486 C; 370 G; 372 T;

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Circle No. 17

Query Match 20.6%; Score 291; DB 10; Length 1821;

Best Local Similarity 70.8%; Pred. No. 5,67e-190;
Matches 597; Conservative 0; Mismatches 234; Indels 12; Gaps 8;

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Db 181 catcacgcgcctactcgcgtgtgtgscgaagtggtggtcctgggaagctgcgcgtcat 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 368 CATCACGCGCTGCTACTCTGCTGGGATTTGGTGGGCTTATGGGCAATTCCTGSGTCAT 427
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 gtttgcatcgtcgcgtacacccaattgaagacgcgcacacacacacacacacacacac 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 428 GTTGTGATCATCGATACACAGAGATGAGACCGCAACACATCTACATATTAACT 487
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 ggccttgatgacgcgtgcgcacacacacacacacacacacacacacacacacacacac 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 488 GCGTTTGCGAGATGCTTGGTGTACTACACATATGCCCTTTGAGAGTGTGTCTATGAT 547
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 ggaagacgtgcgcgttgscgcgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgc 420
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 548 GAATTCCTGGGCTTTGGAGATGCTGATGCAAGATTTGTCATTTCATTGCTACTACACA 607
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 421 catgtcacatcatcaccacacacacacacacacacacacacacacacacacacacacac 480
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 608 CATGTTTACGACGATATTCACACTGACATGATGATGATGATGATGATGATGATGATGATG 667
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 481 ccatctcgtcaaacgcctgcgcacacacacacacacacacacacacacacacacacacac 540
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 668 CCACCTCTGTAAGCTTTGGAATTCGCAACCTTTGAAGCAAGATCATCAATCTG 727
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 541 catctggtctgtgttgatggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 600
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 728 CATTTGGCTCTCCGATATCTGTTGATATACAGCGATAGCTTCTGAGAGGACCAAGT 787
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 601 ccgagatggtcagtggt-at-gcatgtcc---agttccacagtcacagtcgttactg 654
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 788 CAGGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 847
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 655 g-gaca-ctgtg-accacagatcgtgttctctctctctctctctctctctctctctctcat 711
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 848 GTGGGATCTCTTCATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 907
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 712 catcacggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 771
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 908 CATCATGCTGCTCTACACCTCATGATATCTGCGCTGAAAGATGTGTCGGCTCTGCTGCTG 967
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 772 ttccaagagaaagacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 831
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 968 CTCGCGAGAGAGAGACCGAATCTCGCGCAACCAAGCTGAGTGTGATGATGATGATGATG 1027
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 832 cgcctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 891
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1028 AGTCTTCAATCATCTGTTGACCCCATTCATACATCTTTATCTGCTGCTGCTGCTGCTG 1085
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 892 catcacggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 951
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1086 -AGCACTCTCCACAGACACAGCTGCTCTCCAGCTATTTTCTGTGATTTGCTGCTGCTG 1144
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 952 cgcacacagacacacacacacacacacacacacacacacacacacacacacacacacac 1011
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1145 TACCAACAGAGAGCTGAATCTGCTCTATGAGCTTTGAGTGAAGAACTCAAGCGGTG 1204
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1012 cct 1014
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1205 TTT 1207
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 10
ID 075927 standard; DNA; 2272 BP.

AC 075927;
DT 17-AUG-1995 (first entry)
DE Mouse delta oploid receptor MORDL cDNA.
KW Mouse; kappa; delta; mu; oploid receptor; brain; primer; PCR; amplify;
transmembrane domain; somatostatin; receptor; human; expression vector;
truncate; chimera; assay; probe; ss.
OS Mus musculus.

```

FH Key Location/Qualifiers
FT CDS 12..1130
FT /product= mouse delta oploid receptor
FT /tag= a
PN M09428132-A.
PD 08-DEC-1994.
PF 20-MAY-1994; U05747.
PR 20-MAY-1993; US-066296.
PR 30-JUL-1993; US-100694.
PR 05-NOV-1993; US-147592.
PA (ARCH-) ARCH DEV CORP.
PI Bell GI, Reisine T, Yasuda K;
DR P-PSDB; R67870.
PT Polypeptides and peptides derived from oploid receptor
PT screening assays for useful drug substances.
PS Claim 6; Page 215-221; 300pp; English.
CC The nucleotide sequence of the novel mouse delta oploid receptor gene
CC MORDL. The gene was isolated from a mouse brain cDNA library using a
CC fragment (amplified from the cDNA library with primers 075929-30) as a
CC probe. The primers are based on the conserved sequences present in the
CC second and third transmembrane domains of somatostatin (STR) receptor
CC subtypes STR1, STR2 and STR3. The 1.3 kb EcoRI-SacI fragment from the
CC mouse delta oploid receptor clone, lambda ms1-2, was subcloned into the
CC CMV promoter-based expression vector pCMV-6c. The resultant construct
CC pCMV-ms1-2 was transfected into COS-1 cells for protein production. The
CC gene encoding the oploid receptor can be used to produce complete,
CC truncated or chimeric oploid receptor proteins. The oploid receptors
CC thus produced are useful for the development of novel assays designed to
CC select or improve substances, capable of interacting with the oploid
CC receptor proteins, for use in diagnosis, drug design and therapeutic
CC applications.
CC Sequence 2272 BP; 485 A; 665 C; 650 G; 472 T;
SQ

```

Query Match 20.6%; Score 291; DB 13; Length 2272;
Best Local Similarity 70.8%; Pred. No. 5,67e-190;
Matches 597; Conservative 0; Mismatches 234; Indels 12; Gaps 8;

```

Db 164 catcacgcgcctactcgcgtgtgtgscgaagtggtggtcctgggaagctgcgcgtcat 223
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 368 CATCACGCGCTGCTACTCTGCTGGGATTTGGTGGGCTTATGGGCAATTCCTGSGTCAT 427
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 224 gtttgcatcgtcgcgtacacccaattgaagacgcgcacacacacacacacacacacacac 283
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 428 GTTGTGATCATCGATACACAGAGATGAGACCGCAACACATCTACATATTAACT 487
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 284 ggccttgatgacgcgtgcgcacacacacacacacacacacacacacacacacacacacac 343
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 488 GCGTTTGCGAGATGCTTGGTGTACTACACATATGCCCTTTGAGAGTGTGTCTATGAT 547
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 344 ggaagacgtgcgcgttgscgcgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgc 403
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 548 GAATTCCTGGGCTTTGGAGATGCTGATGCAAGATTTGTCATTTCATGATGATGATGATGATG 607
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 404 catgtcacatcatcaccacacacacacacacacacacacacacacacacacacacacacac 463
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 608 CATGTTTACGACATTTACCTTGACATGATGATGATGATGATGATGATGATGATGATGATG 667
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 464 ccatctcgtcaaacgccttgacatccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 523
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 668 CCACCTCTGTAAGCTTTGGAATTCGCAACCTTTGAAGCAAGATCATCAATCTG 727
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 524 catctggtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 583
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 728 CATTTGGCTCTCCGATATCTGTTGATATACAGGATATGCTTTGAGAGCACCAAAAGT 787
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 584 ccgagatggtcagtggt-at-gcatgtcc---agttccacagtcacagtcgttactg 637
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 788 CAGGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 847
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 638 g-gaca-ctgtg-accacagatcgtgttctctctctctctctctctctctctctcat 694
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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QY 848 GTGGGATCTCTTCATGAGATCTGTGTCCTTTCCTTTGCTTTTGATGCCAGTCTCAT 907
DB 695 catcaagctgtgcatatgagccctcatgctactgagcgtcgcagagctgtgctgtccgg 754
QY 908 CATCATGTGTGTCTACACACCTGTGATGCTGCGCTGAAGAGTGTCCGGCTCTCTGTGG 967
DB 755 ttccaagaaagagaccgagcgtcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 814
QY 968 CTCCTCGAGAGAGACCGAATCTCCCGCATCCACCAACTGGTGTGTGTGTGTGTGTGTGT 1027
DB 815 cgccttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 874
QY 1028 AGTCTTCATATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1085
DB 875 catcaatcgagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 934
QY 1086 -ACCACTCTCCACACACACACTGCTCCCTTCACACTATATTTCTGTGTGTGTGTGTGT 1144
DB 935 cgcacaagagagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 994
QY 1145 TACCACAGAGAGCTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1204
DB 995 ctt 997
QY 1205 TTT 1207

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RESULT 11

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ID 089226 standard; cDNA: 1610 BP.
AC 089226;
DT 20-OCT-1995 (first entry)
DE Human mu opioid receptor cDNA.
KW Mu opioid receptor; MOR; gene therapy; diagnostic; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 239..1441
  /tag= a
  PN W09507983-A.
  PD 23-MAR-1995.
  PE 13-SEP-1994: U10358.
  PR 13-SEP-1993; US-120601.
  PA (INDV ) UNIV INDIANA FOUND.
  PY Yu L;
  DR WPI; 95-131351.17.
  DP P-PSDB; R71966.
  PT New nucleic acid encoding new human mu opioid receptor - and
  PI related vectors, transformed cells, antibodies etc., useful in
  PS diagnosis, treatment and drug screening.
  PS Claim 5; Page 208-210; 265pp; English.
  CC A cDNA library constructed from human candidate nucleus mRNA was
  CC screened with rat mu opioid receptor cDNA under conditions of
  CC low stringency. One positive clone included the sequence given in
  CC 089226, encoding a mu opioid receptor MOR (R71964). The cDNA
  CC is used for prodn. of recombinant MOR, in gene therapy, etc.
  SQ Sequence 1610 BP; 384 A; 467 C; 359 G; 400 T;

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Query Match 20.5%; Score 289; DB 14; Length 1610;

Best Local Similarity 70.0%; Pred. No. 1,77e-188;

Matches 601; Conservative 0; Mismatches 246; Indels 11; Gaps 10;

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DB 455 atcatggccctactcatcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 514
QY 369 ATCACCGCTGTCTACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 428
DB 515 tatgtgatctgaatatacacaagaatgaagctgcacacacatataatttcaactt 574
QY 429 TTTGTCATCATCGATACAGAAAGATGAAGACCGCAACCAATATATTTTAACTGT 488
DB 575 gctctggagatgctttagcaccacagatccctgcctccagagtgttaataactaagt 634
QY 489 GCTTTGGAGATGCTTTGGTACTACACTATGCCCTTTCAGAGGCTGTCTACTTGTATG 548
DB 635 ggaacatgagcatgtgaaacacatccttgcaagatagatgactcctcatagattactataac 694

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QY 549 AATCTTGGGCTTTTGAGATGTGCTATGCAGAAATGTCTATTTCCATTGACTCTCTACAC 608
DB 695 atgttcaaccagatattacacccctcgcacacatgaagtgttatcgataacattgaagctcgc 754
QY 609 ATGTTTACAGCAATTCATCTTACACCTTGACCATGATGATGATGATGATGATGATGATGATG 668
DB 755 caacctgtcaaggccttagatllccgtaactccccgaatgccaataatcaatgctgtgc 814
QY 669 CACCTGTGAAGCTTTGGACTTCCGACACCTTTGAAGCAAGATCATATCATCTGTGC 728
DB 815 aactgtatcctctctcgaacatggctcctcgtatgtaatgtatgtaataaataaataac 874
QY 729 ATTGTGCTCTGTCATCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 788
DB 875 aggcagagt-tcatag-attgta--cac-taacattc-c-loatcaactgtgactcg 928
QY 789 AGGGAAGATGTGATTCATATGATCTCTCTGCACTTCCATTTCTGATGATGATGATGATGATG 848
DB 929 -gaaac-ctgc-tgaagatctgtttcaatcttgsccttccttataagcagtgctcgc 985
QY 849 TGGGATCTCTCATGTAAGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 908
DB 986 attaccgtgtgctatgagactgagatcttgagcctcaagaagtgcgcagctctctgcgc 1045
QY 909 ATCATGTGCTGTACACCTGTGATGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 968
DB 1046 tccaaagaaagagacagagatcttgaagatcacacagagatgtgtgtgtgtgtgtgtgt 1105
QY 969 TCCCGAGAGAGAGCCGAATCTCCGCGCATCACCAACCTGTGTGTGTGTGTGTGTGTGTGTGT 1028
DB 1106 gtttcaatcgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1165
QY 1029 GTCTTCATCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1088
DB 1166 atccagaagactac-gttccagactgttctgtgacactgtcattgtcctatgattac 1224
QY 1089 ACCTCCACAGACAGACGCTCCCTCTCCAGCATAT-ATTTCGTATTTGCTTGGTTATAC 1147
DB 1225 aacagctggcctcaaccccaagctcttatgcatcttctgtatgataaactcaacagatgctt 1284
QY 1148 CACACAGACGCTGAAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1207
DB 1285 cagagagttcgtatccc 1302
QY 1208 TGGGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1225

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RESULT 12

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ID 093102 standard; cDNA: 2160 BP.
AC 093102;
DT 11-DEC-1995 (first entry)
DE Human mu opiate receptor cDNA.
KW Mu opiate receptor; hMOR; opiate agonist; opiate antagonist;
  drug abuse; analgesic; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 213..1415
  /tag= a
  PN W09520667-A1.
  PD 03-AUG-1995.
  PE 30-JAN-1995: U01144.
  PR 28-JAN-1994; US-188275.
  PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
  PI (USSH ) SEC DEPT HEALTH.
  DR Johnson PS, Persico AM, Uhl G, Wang J;
  DP WPI; 95-275452/36.
  DP P-PSDB; R76780.
  PT New DNA encoding human mu opiate receptor - used esp. for screening
  PT ops. for activity as opiate agonists or antagonists
  PS Claim 4; Page 24-25; 49pp; English.
  CC hMOR cDNA was obt'd. from a human cerebral cortical cDNA library
  CC screened with fragments of a rat mu opiate receptor. Cloned hMOR

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[illegible]

RESULT	15	
ID	Q089233	standard; CDNA; 1567 BP.
AC	Q089233;	
DE	20-OCT-1995	(first entry)
DE	Rat opioid receptor CDNA	
KW	Opioid receptor; MOR-1; gene therapy; diagnostic; ss.	
OS	Rattus sp.	
EH	Key	Location/Qualifiers
FT	CDS	173..1276
FT	/*tag= a	
PN	W09507983-A.	
PD	23-MAR-1995.	
PE	13-SEP-1994; U10358.	
PR	13-SEP-1993; US-120601.	
PA	(INDV) UNIV INDIANA FOUND.	
PI	YU L.	
DR	WPI; 95-131351/17.	
DR	P-PsDB; R71968.	
PT	New nucleic acid encoding new human mu opioid receptor - and	
PT	related vectors, transformed cells, antibodies etc., useful in	
PT	diagnosis, treatment and drug screening.	
PS	Example 9; Page 218-222; 266pp; English.	
CC	The CDNA given in Q089233 was isolated from a rat brain library by	
CC	low stringency hybridization with rat mu opioid receptor CDNA	
CC	(Q089222). The clone encoded a 367-amino acid protein (R71968)	
CC	that showed high homology with mu, kappa and delta opioid receptors	
CC	but lacked affinity for their ligands, suggesting it to be	
CC	a novel member of the opioid receptor family.	
Sequence	1567 BP;	313 A; 440 C; 402 G; 412 T;

